STIC-Biotech/ChemLib

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Whiteman, Brian

Sent:

Monday, January 30, 2006 3:14 PM

To:

STIC-Biotech/ChemLib

Subject:

seq search

10/069386

SEQ ID NOs: 1 and 2 1) interference search

2) us patent and published us patent application databases

Thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

(S110)

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
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Type of Search

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source unidentified unidentified unclassified AX088925 Sequence 1 AX088925 AX088925.1 Alaoui-Jamali, M.A. and Cho, J.M. Replication protein a binding transcriptional uses thereof Patent: WO 0114546-A 1 01-MAR-2001; Centre for Translational Research in Cancer (C : WO 0114546-A 1 01-MAR-2001; for Translational Research in Location/Qualifiers /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" /note="replication protein from Patent GI:13397684 sequences 591 bp WO0114546. DNA Þ transcriptional linea (CA) factor PAT (rbt1)factor" 17-MAR-2001

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ACCCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTGCCCCCGAG

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Cho, J.M., Song, D.J. and Alaoui
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Institute, 3999 Cote-Ste-Cathe
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RBT1, a novel transcriptional co-activator, subunit of replication protein A Nucleic Acids Res. 28 (18), 3478-3485 (2000)
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/gene="RBT1"
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/product="RPA-binding trans-activator"
/protein_id="AAF05761.1"
/protein_id="AAF05761.1"
/db_xref="GI:6180045"
/translation="MEGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRS
/translation="MEGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRS
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                           Homo sapiens (human)
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Mammalia; Eutheria; I
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Ota, T., Nii
Wakamatsu, J
Koga, H.
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Bu,A., Sugiyama
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for synthesizing full-length cDNA and use the Location/Qualifiers (93)...(680).
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/organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Local Similarity 99.8%;
nes 590; Conservative
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to Homo sap
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oligo cappi
Homo sapien
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Patent: EP 1396543-A 4084 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
93. .683
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/protein_id="CAF86937.1"
/protein_id="CAF86937.1"
/db_xref="GI:45503846"
/translation="MVGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRS
/translation="MVGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRS
LGPRAPSLRRHVLIHNTLQQLQAALRLAPAPALPPEPLFLGEEDFSLSATIGSILREL
DTSMDGTEPPQNPVTPLGLQNEVPPQPDPVFLEALSSRYLGDSGLDDFFLDIDTSAVE
KEPARAPPEPPHNLFCAPGSWEWNELDHIMEIILGS"
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hes 590; Conservative
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Unpublished

(bases 1 to 1325)

(bases 1 to 1325)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA library construction:

Institute of Medical Science, University of Tokyo, Laboratory of

Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass

sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Isogai, T., Ota, T., Nishik
Sugiyama, T., Suzuki, Y., N
Kawai-Hio, Y., Saito, K., Y
Kojima, S., Nagahari, K., M
Aotsuka, S., Sasaki, N., Ha
Ninomiya, K.
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S Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shanmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TM Mammallan Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
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This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 1 Location/Qualifiers
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1 (bases 1 to 1420)

2 Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RP, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Pahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

RTM Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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D 12477932

E (bases 1 to 1420)

E Director MGC Project.

Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

Trastitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

Trastitute (1420)
                                                                                                                                                                                                                                                                                                                                                                                                                  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:29791864.

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: //www-shgc.stanford.edu
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ickson, Mark) mcd@paxil.stanford.edu
Schmutz, J., Grimwood, J., Rodriquez,
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/note="Vector: p
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int: WO 02068579-A 17487 06-SEP-2002;
corporation (NY) (US)
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                                                  GGAGCCTGCACGGGCCCCACCAGAGCCTCCTCACAACCTCTTCTGTGCCCCCAGGTTCT
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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DNA linear PRI 13-JUL-2002 CTC-492K19, complete sequence.

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Submitted (13-JUL-2002) DOE Joint Genome Drive, Walnut Creek, CA 94598, USA
On Jul 13, 2002 this sequence version reduced by DOE Joint Genome Draft Sequence Produced by DOE Joint Genome www.jgi.doe.gov
Finishing Completed at Stanford Human Genome www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence Phrap Phra
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Submitted (15-SEP-1999) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
|chromosome="19"
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Primer for Synthesizing full-length cDNA and use thereof
Primer for Synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 121 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/121
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/00 CC
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for Synthesizing full-length cDNA and use thereof FH Key
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Primer for
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JP 20020173
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Mammalia; Eutheria;
                        AAGGAGCCTGCACGGGCCCCACCAGAGCCTCCTCACAACCTCTTCTGTGCCCCCAGGTTCT
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ACCCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTGCCCCCGAG
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,T., Nishikawa,T., Isogai,T., Hayashi,K., Ish
amatsu,A., Sugiyama,T., Nagai,K., Kojima,S.,
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002017375-A/121.
sapiens (human)
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her for synthesizing full-length cDNA and use thereof FH 1
Location/Qualifiers
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larity 99.7%;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Primer fo
BD126646
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Primer for synthesizing full-length cDNA and Patent: JP 2002017375-A 2077 22-JAN-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2077
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1 (bases 1 to 825)
1 (bases 1 to 825)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Kojima,S.,
                                                                                                                                                                               H.H.
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JP 2002017375-A/2077.
Homo sapiens (human)
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PI TETSUJI OTI
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Mammalia; Eutheria;
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          Similarity
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ner for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
source 1. .825
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07-JUL-2000 JP
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                                                                                organism="Homo sapiens/mol_type="genomic DNA"/db_xref="taxon:9606"
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        99.6%;
99.7%;
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SUO NISHIKAWA, TAKAO
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Euarchontoglires; P
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Pred.
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        588.4; DB 6;
No. 3.1e-113;
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Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                 SUGIYAMA, KBIICHI
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T. and
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1 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y. Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 121 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; F
Hominidae; Homo.

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Wakamatsu, A., Sugiyan
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COMMENT

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Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 28, 2000 this sequence version replaced gi:6705474 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps runs of N, but This record wil as soon as it i be preserved.
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Center clone name: 384 B 6

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 145359 bases at least Q40

Consensus quality: 155420 bases at least Q30

Consensus quality: 159351 bases at least Q20

Insert size: 161352; sum-of-contigs

Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' se consists of 34 contigs. The true is not known and their order in tarbitrary. Gaps between the conti
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.center project Information
Center project name: L5880
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ALIGNMENTS

AAF2805 RBT1; replic gene therapy LT 1 8052 AAF28052 Key WO200114546 Unidentifie Replication 23-MAY-2001 AAF28052; 38 -A2. cation protein A binding transcriptional activator 1; RPA32; y; apoptosis; cancer; leukaemia; ds. andard; DNA; 591 BP. protein A binding transcriptional activator 1 RBT1 gene. (first entry) 1. .591 /*tag= a /product= "RBT1" Location/Qualifiers

01-MAR-2001

17-AUG-2000; 2000WO-CA000948.

19-AUG-1999 99US-0149472P.

(TRAN-) CENT TRANSLATIONAL RES IN CANCER.

Alaoui-Jama li MA, Cho JM;

WPI; 2001-21 P-PSDB; AAB3 218447/22. 335402.

Novel replication protein A binding transcriptional activator 1 gene, useful for treating neoplastic disorders such as cancer and in gene therapy.

Claim 1; Ħ 1; 16pp; English.

The present invention provides the protein and coding sequences of the

Ishii S, S, Otsuki

Kawai Y; T, Koga

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P-PSDB;
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Sugiyama T, Nagai
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Pred. No. 1.4e-134;
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K, Kojima S,
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02-MAY-2000;
07-JUL-2000;
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Wakamatsu A, Sugiyama
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide nucleotide sequences; (b) an amino acid sequence encoded by any of the above length coding region of the above nucleotide sequences; or (c) a sequence
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comprising the above polypeptide fused to a heterologous polypeptide; (6) can isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (7) a process composition of matter comprising the above polypeptide; (7) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter contained within the container; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth cells that express the above protein; (13) a method of cells that expresses the above protein (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a cancercous tumour in a composition and (17) a method of binding an antibody, oligopeptide or composition and method of binding an antibody, oligopeptide or composition and method of binding an antibody, oligopeptide or composition and method are useful for diagnosing, containing the presence of a cell proliferative disorder. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The composition detection of a cell for preparing the cell proliferative disorder or cancer. The composit
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Sequence 1515 BP, 328 A; 404 C; 385 ູດ 398 T; 0 ď, 0 Other;

Query Ma Best Loc Matches

Local

ch 99.7%;
Il Similarity 99.8%;
590; Conservative

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Score 589.4; DB 13 Pred. No. 1.5e-134;); Mismatches 1;

Indels

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Gaps

WPI;

2003-8

77243/81.

Wohlgemuth

Fry K,

Woodward R,

Ly N;

(EXPR-)

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INC.

DB 13;

Length

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Match

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Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one more genes. 9

Claim 18; S EQ ID NO 451; 877pp; English.

This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus of erythematosis (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma, ankylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This polynucleotide is a DNA sequence representing human mRNA that is of the invention ankylosing s cholangitis, This polynuc differential of the inven ntion.

15 42 BP; 346 A; 405 C; 388 G; 403 T; 0 U; 0 Other;

Ş 멍 ঠ Query Match Best Local s Matches 590 292 61 ۳ Similarity 90, Conserv =;; GAGTCCAGCAGGCCTTCAGAGCTACCAGCAAGCCCTGCTCCGCATCTCCCTAGACAAA Conservative 99.7**%**; 99.8**%**; 0 Score 589.4; DB 10; Pred. No. 1.5e-134; 0; Mismatches 1; Indels Length 1542; 0 Gaps 120 351 60 <u>0</u>

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The invention relates to providing a patient diagnosis for lung cancer comprising comparing the level of expression of genes or gene products a biological sample from the patient with the level of expression of genes or gene products in a biological sample from a normal individual Also included are distinguishing between normal and disease tissues,
                                                                                                                                                                                    Claim
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Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refer to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a methofor efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is the 5' end of a full length human cDNA sequence of the invention.
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expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes for measuring human gene expression, a method of measuring human gene expression, a method of contiguous amino acids of any of the above - mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, in ORF-encoded peptide exon probes or microarrays to measure gene expression, a method of sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, an of the above - mentioned amino acid solated antibody that binds specifically to a peptide cited above, and or licensing single exon probes or microarrays to storage medium which contains a database having a plurality of records cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying their segments to detect the presence of expressed messages that contain their
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                                             The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), cor antigen presenting cells that express (II). (I) has cytostatic carriers an cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide (IV) and comparing the amount of polynucleotide hybridising to (IV) is detected preferably cancer and thereby detecting ovarian cancer in the patient, where the computer of polynucleotide hybridising to (IV) is detected preferably by colymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian thmour protein comprising contacting T cells specific for an ovarian captulating and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA contacting techniques
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               for therapy and diagnosis of ovarian cancer comprising of a ovarian tumor polypeptide, polynucleotide encoding antibody specific to polypeptide or T cell expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic carriers are carrier in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide tybridising to (IV) and comparing the amount of polynucleotide amount of polynucleotide hybridising to (IV) is detected preferably by colymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian cuseful in design and preparation of ribozyme molecules for inhibiting capression of the tumour polypeptides and proteins in tumour cells; and consolate a full length gene from a suitable library e.g., a tumour cDNA is comparaty using well known techniques
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially and daressable set of single exon nucleic acid probes for measuring human gene expression, a plurality of single exon nucleic acid grobes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of probes cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid substitutions), an acc isolated antibody that binds specifically to a peptide cited above, an customer desiring to measure gene expression, a method of providing the man gene expression and acid substitutions, an a customer desiring to measure gene expression, a method of providing thuman gene expression and the acomputer-readable exon probe cited above. The probes methods and apparatus are useful in gene expression analysis. The probes and apparatus are useful in gene expression analysis. The probes and apparatus are useful in gene expression analysis. The probes and apparatus are useful in their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are useful indentifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising specific acids, in a seessing single exon probe of the in
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ALIGNMENTS

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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandala
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling
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Nat. Biotechnol. 22 (6), 707-716 (2004)
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling network control human ES cell growth and differentiation
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                                                             bases 1 to
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/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENBU"
/note="oligo dT_primed, full-length enriched cDNA library from hBS cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                  ; Metazoa;
Eutheria;
                                                                        Homo.
                                                               742)
                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 2.1e-135;
); Mismatches 1;
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16-MAY-2004

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230 Constitution Drive, Menlo Par
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 742 Std Error: 0
Location/Qualifiers
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Contact: Brandenberger F
Regenerative Medicine
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ilarity 99.8%;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic s
line"
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/note="oligo dT_primed, full-length
from DMSO-treated hES cell line H9 (
feeder-free conditions"
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NIH_MGC_119 Homo
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12766 row: i column: 08
High quality sequence start: 32
High quality sequence stop: 703.
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                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5744719"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;

Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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Eutheria;
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Matches 590; Conservative
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1298)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR605181 1298 bp mRNA full-length cDNA clone CS0DJ012YJ05 of T Cot 10-normalized of Homo sapiens (human) CR605181 CR605181.1 GI:50485988 HTC; CNSLT_cDNA.
                                                                                                                                        μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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sapiens (human)
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ012YJ05"
/tissue_type="T cells (Ju:
10-normalized"
/plasmid="pCMVSPORT_6"
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Contact : Fe
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//fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/mol_type="mRNA"

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National Institutes of Health, Mammalian Gene Collection (Mational Institutes of Health, Mammalian Gene Collection (Mammalian Gene Collec
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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/clone_lib="NIH_MGC_110"
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/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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Best Local Similarity 99.8%;
Matches 581; Conservative
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Geron Corporation
230 Constitution Drive, M
Tel: 650 473 8658
Fax: 650 473 7760
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1 (bases 1 to 646)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,GLi,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

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TGGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTG
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Length: 646 Std Error:
Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_prENEU"
/note="oligo dT_primed, full-length enriched cDNA library
/note="oligo dT_primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."
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On May 13, 2003 this sequence version replace Contact: Genoscope
Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
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p://www.genoscope.cns.fr/cdna?s=CSODIO57BG07QP1&c=9131.r.
Location/Qualifiers
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alia; Eutheria;
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sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mkNA"
/db_xref="taxon:9606"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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mol_type="mRNA"
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B & B &	Query Ma Best Loc Matches	ORIGIN	FEATURES sour	TITLE JOURNAL PUBMED COMMENT	REFERENCE AUTHORS	LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db RESULT 10 CN304594	Qy Db	\$ \$ \$ \$
1 ATGGAGGGAGGCTTGAAGAGGAAACACTCTGATTTGGAAGAGAGAG	97.3%; Score 575.2; DB 7; Length 712; cal Similarity 99.3%; Pred. No. 6.9e-132; 588; Conservative 0; Mismatches 3; Indels 1; Gaps 1;		oration Dri tution Dri 73 8658 73 7760 andenberge gth: 712 ocation/Qu	Transcriptome characteriza control human ES cell grow Nat. Biotechnol. 22 (6), 7 15146197 Contact: Brandenberger R	nordat uarcho ,H., Z ,Gueg	CN304594 712 bp mRNA linear EST 16-MAY-2 17000532611443 GRN_EB Homo sapiens cDNA 5', mRNA sequence. CN304594 CN304594.1 GI:47321008 EST. Homo sapiens (human) 1 Homo sapiens	541 TGGGAGTGGAATGAACTGGATCATCATGGAAATCATTCTGGGGTCCTAA 591	531 TACTTGGGGGACTCTGGCCTGGATGACTTCTTTCTGGACATTGACACATCTGCGGTAGAA 590 481 AAGGAGCCTGCACGGGCCCCACCAGAGCCTCCTCACACACCTCTTCTGTGCCCCAGGTTCT 540	411 GAGCTGGACACCTCCATGGATGGACTGAGCCCCCTCAGAATCCAGTGACTCCCCTTTGGC 470 361 CTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCGG 420 [
	FEATURES source	JOURNAL	SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE	LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Db 6 RESULT 11 RESULT 11		Q D Q D	Q Q 2	Qy 1 Db 2 Db 1
/db xref="taxon:9606" /clone="IMAGE:6503515" /tissue_type="leiomyosarcoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_71" /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "	=	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14061 row: e column: 20	Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 873) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	BU508982 BU508982 BU508982 AGENCOURT_10095430 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6503515 5', mRNA sequence. BU508982 BU508982.1 GI:22815215	540 TIGGGAGIGGAACIGGAICACAICAIGGAAAICAITCIGGGGICCIAA 591 		CATGGATGGGACTGAGCCCCTCAGAATCCAGTGACTCCCCTTGGC 47 CCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTCTGAGCTCCCCGG 42 CCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCGG 53 CCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCCGG 53 CTGGCCTGGATGACTTCTTTCTGGACATTGACACCATCTGCGGTAGAA 48	241 CCCCTCTTCCTGGGCGAGGAGGATTTCTCCCCTGTCAGCCACCATTGGCTCTATCCTCAGG 300	121 GTCCAGCGCAGCCTGGGCCCCCGAGCACCCAGCCTCCGCAGGCATGTCCTCATCCATAAC 180

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    Genome Biol. 6 (7), R60 (2015998449)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 4
Tel: 2063780400
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1 (bases 1 to 970)

Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B., Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. Iadonato,S.P.

Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005)
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ILLUMIGEN MCQ 49981 Katze MMIL Macaca mulatta cDNA clone IBIUW:19438 5' similar to Bases 114 to 970 highly similar SERTAD3 (Hs.169138), mRNA sequence.

CO579535

CO579535.1 GI:50410495

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Macaca mulatta
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Pred. No. 4.9e-130;
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Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 648 Q20 bases. Library Preparation: Pro
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR PRimers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 970 Std Error: 0.00
Plate: CL000412 row: B column: 10
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
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/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:19438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMIL"
/note="Organ: ileum; Vector: pDONR 222;
Site_2: BsrG I; Created from CloneMiner
Construction kit (catalog #18249-029)"
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Pred. No. 2.8e-128;
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Site_1: BarG cDNA Library

Gaps

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10736 row: a column: 09
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National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Butheria;
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                                                                                                               ACCCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGGCCCCTGCCCCTGCCCCCGAG
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primer
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/note="Organ: testis; Vector: pBluescriptR (modified
/note="Organ: testis is a primer
/clone="IMAGE Library organics primer
/clone="IMAGE Library organics primer
/clone="IMAGE Library."
/clone="IMAGE: A824464"
/clone="IMAGE: Library organics primer
/clone="IMAGE: Site_1"
/clone="IMAGE: A824464"
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/clone="IMAGE: A824464"
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(gtcgag); Oligo-dT primed using primer
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/clone="IMAGE: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
/clone="IMAGE: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
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mol_type="mRNA"

db_xref="taxon:9606"
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On May 5, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                             For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DJ012CE03QP1&c=9131.r. Location/Qualifiers
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Homo sapiens cDNA clone
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Mammalia; Eutheria;
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ue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
il: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
enriched, double-strand cDNA was digested with Not I and cloner
o the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
normalized. Library was constructed by Life Technologies, a
ision of Invitrogen. This sequence belongs to sequence cluster
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                                                                               /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                             cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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                                                                                                                                                 0-NORMALIZED"
                                                                                                                                                                                                                                                               organism="Homo sapiens"
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Score 558; DB pred. No. 1.4e l; Mismatches
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1.4e-127;
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ATGGAGGGAGGCTTGAAGAGGAAACACTCTGATTTGGAAGAGGAGGAGGAGGAGGTGGGAG

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RESULT 15
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TITLE
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                                                                                                                                                                                                                                                                                  ORGANISM
                          Bourc
                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12709 row: j column: 09
High quality sequence start: 20
High quality sequence stop: 626.
Location/Qualifiers
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5', mRNA 8
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1 (bases 1 to 1045)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
Unpublished (1999)
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Mammalia; Butheria;
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_type="mRNA"
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/clone="IMAGE:5722856"
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Sequence
Patent No
GENERAL
IELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ~~~
                                                                                                                                                            STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313
PFLING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMP
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

TINFORMATION FOR SECIED NO: 14:
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atent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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CURRENT APPLICATION NUMBER: US/10/076,0
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JURECIC, ROLAND
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7001ence 12197,
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US-09-949-016-17583/c
; Sequence 17583, Applia
; Patent No. 6812339
; GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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NUMBER OF SE
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                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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APPLICATION NUMBER: 60/237,768
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US-09-733-294A-30/c
; Sequence 30, Application U
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
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CURRENT APPLICATION NUMBER: US/09/73
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
                                                                                                                                                                                           NUMBER
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TITLE OF INVENTION: ANTISENSE MODULATION
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LOCATION: (12951)...(21566)	OTHER INFORMATION: intron 2	NAME/KEY: exon
LOCATION: (21567)...(21762)	OTHER INFORMATION: exon 3	NAME/KEY: intron
LOCATION: (2163)...(23851)	OTHER INFORMATION: intron 3	NAME/KEY: intron
LOCATION: (23852)...(24032)	OTHER INFORMATION: exon 4	NAME/KEY: exon
LOCATION: (24033)...(24719)	OTHER INFORMATION: intron 4	NAME/KEY: intron
LOCATION: (24720)...(24899)	OTHER INFORMATION: exon 5	NAME/KEY: exon
LOCATION: (24720)...(24899)	OTHER INFORMATION: intron 5	NAME/KEY: exon
LOCATION: (25394)...(25549)	OTHER INFORMATION: exon 6	NAME/KEY: exon
LOCATION: (25394)...(30196)	OTHER INFORMATION: exon 6	NAME/KEY: exon
LOCATION: (25394)...(30196)	OTHER INFORMATION: exon 7	NAME/KEY: exon
LOCATION: (31059)...(31059)	OTHER INFORMATION: exon 9	NAME/KEY: exon
LOCATION: (31359)...(31359)	OTHER INFORMATION: exon 1	OTHER INFORMATION: exon 1

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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,698
                                                                                      SEQ ID NO
LENGTH:
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Best Local S
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NAME/KBY: intron
LOCATION: (46255)...
OTHER INFORMATION: i
                                                                                                                      SOFTWARE:
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TITLE OF INVENTION: HUMAN CDNAS
FILE REFERENCE: 91.US6.DIV
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                                                                                                                                     NUMBER OF
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LOCATION: (47710)...
OTHER INFORMATION: e
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LOCATION: (47036)..
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 NAME/KEY:
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APPLICATION NUMBER: US
FILING DATE: 2001-05-25
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GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: METHOD FOR MAINTENANCE
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
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NAME/KEY:
LOCATION:
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NAME/KEY: CDS
LOCATION: (1)..(1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA
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US-09-410-399-3/

Sequence 3, Patent No.

Application US/09410399 6482587

RESULT

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US-09-050-863-2/c
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Best Local
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                                                                                                                                                              COUNTRY: USA-
COUNTRY: USA-
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
Delease #1.0,
                                                      COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-I SOFTWARE: Patentin Release # CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/05 FILING DATE: 30-MAR-1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M. REGISTRATION NUMBER: 38,304 REFERENCE/DOCKET NUMBER: A-6
TELEFAX: (415) 949-871 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin
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TITLE OF INVENTION:
FILE REFERENCE: UM-
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TYPE: DNA
ORGANISM: Epstein-Barr
                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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DF SEQ ID NOS: 6
3: PatentIn Ver. 2.0
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Pred. No.
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Patent No. 6316223
GENERAL INFORMATION:
CANT: Lao, Ying
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Matches 95
                                                                                                                                                                                                            INFORMATION
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MOLECULE TYI
9-050-863-2
                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Ju1-1999
CLASSIFICATION NUMBER: 09/050,863
PILING DATE: <Unknown>
PRIOR APPLICATION NUMBER: 09/050,863
FILING DATE: <Unknown>
AFTTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 949-8711
FORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
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STRANDEDNESS: unknown
MOLECULE
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Similarity 51.4%;
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CITY: San
STATE: CA
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ZIP: 9411
                                                                                     TYPE: nucleic acid
STRANDEDNESS: unknown
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      DESCRIPTION:
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Payan, Don
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Sequence 1, Application US/09130114;
Patent No. 5976807;
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Ger;
TITLE OF INVENTION: From Multiple Transfected Episomes;
FILE REFERENCE: 0867/1D903US1;
CURRENT APPLICATION NUMBER: US/09/130,114;
CURRENT FILING DATE: 1998-08-06
                                                                    RESULT 12
US-09-647-344A-14
; Sequence 14, Applicat;
; Patent No. 6586180
; GENERAL INFORMATION:
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                      APPLICANT: Ruffner,
APPLICANT: Pierce,
    APPLICANT:
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ORGANISM: VEBNA
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CURRENT APPLICATION NUMBER: US/09/647,344A; CURRENT FILING DATE: 2000-12-04; PRIOR APPLICATION NUMBER: PCT/US99/06742; PRIOR FILING DATE: 1999-03-28; NUMBER OF SEQ ID NO 14; LENGTH: 8705
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: I
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                                                  TELEFAX: INFORMATION 1
                                                                          APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,45
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                    ZIP: 94608-2916
COMPUTER READABLE FC
MEDIUM TYPE: Flop
COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patent
                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                         LENGTH:
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CITY: 1
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TYPE: nucleic STRANDEDNESS:
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          t: (510) 655-3542
FOR SEQ ID NO: 1
CHARACTERISTICS:
9600 base pairs
nucleic acid
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ilarity 51.4%;
Conservative
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4560 Horton Street
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                                                                              ION INFORMATION: (510) 923-2706
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                                                                                                                    38,459
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Pred. No. 0.92;
0; Mismatches
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-910-647-1
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US-09-620-925-1/c
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GENERAL INFORMATION:
APPLICANT: Zuck
       Best Local Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,647
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       TELECOMMUNICALIC.
TELEPHONE: (510) 923-2700
TELEFAX: (510) 655-3542

DRMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
TYDE: nucleic acid
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                                                                                                                                                                           MOLECULE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Fujita, Sharon M.

REGISTRATION NUMBER: 38,459

REFERENCE/DOCKET NUMBER: 1218.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 923-2706

TELEFAX: (510) 655-3542
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STATE: California
                                                                                                                                                                         TOPOLOGY: linear ULE TYPE: DNA (gonce DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4560 Horton
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6.9%;
ilarity 51.4%;
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B: Chiron Corporation
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 Score 41; DB 3
Pred. No. 0.95;
0; Mismatches
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LEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 15

SEQUENCE CHARACTERISTIC

LENGTH: 10596

TYPE: NICT
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APPLICANT:
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NAME: Dreger, Ginger R.
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FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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ET: 460 Point San Bruno Blvd
South San Francisco
E: California
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UM TYPE: 5.25 inch, 360 Kb fl
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
WARE: patin (Genentech)
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VENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
EQUENCES: 21
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Sequence 40850, A	Sequence 1, Appli	ce 1, App	e 3895, A	Sequence 69519, A	Sequence 27296, A	Sequence 39088, A	9087,	Sequence 39088, A	Sequence 39087, A	498	1	Sequence 71, Appl	1,	1, App	μ,	Sequence 71, Appl	Sequence 71, Appl	Seguence 71, Appl	Sequence 71, Appl	Sequence 53188, A	Sequence 10, Appl

ALIGNMENTS

RESULT 1 US-10-029

9-38 1ce 2

36-2 489

.4898 08, Application US/10029386 00. US20030194704A1

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Sequence 24898, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXTITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2; CURRENT APPLICATION NUMBER: US/10/029,386; CURRENT FILING DATE: 2001-12-20; NUMBER OF SEQ ID NOS: 34288; SOFTWARE: Annomax Sequence Listing Engine vers. 1. SEQ ID NO 24898; LENGTH: 598
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Matches
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010271.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.64
OTHER INFORMATION: EST HUMAN HIT: BG720189.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: O70622, EVALUE 2.30e-01
OTHER INFORMATION: NT HIT: gil6178011, EVALUE 0.00e+00
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CCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTG-CCCCCGA
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ilarity 99.7%;
Conservative
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Pred. No. 4.1e-161;
); Mismatches 1;
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer As

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 1239

LENGTH: 1596
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US-10-106-698-1239
; Sequence 1239, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
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NAME/KEY: misc feature LOCATION: (57)...(57)
OTHER INFORMATION: n equ-10-106-698-1239
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il Similarity 99.3%;
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US-09-867-701-6064
; Sequence 6064, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6064
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-6064
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Pred. No. 6.9e-130;
); Mismatches 5;
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APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAP

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6239
                                                                                                                                              RESULT 5
US-10-029-386-11178
; Sequence 11178, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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US-09-867-701-6239
; Sequence 6239, Application
; Patent No. US20020132237A1
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       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EX.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.
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ORGANISM: Homo
-09-867-701-6239
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APPLICANT: Jones,
ADDITIONAT: Harloch
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ID NO
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Local Similarity 97.1%;
hes 201; Conservative
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Pred. No. 4.8e-45;
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APPLICANT: NACHTMAN, RONALD
TITLE OF INVENTION: HEPP, A NOVEL GENE WITH
FILE REFERENCE: 39532-176599
CURRENT APPLICATION NUMBER: US/10/076,069
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 166
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
FEATURB:
NAME/KEY: CDS
LOCATION: (191)..(901)
3-10-076-069-1
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TYPE: DNA
ORGANISM: Homo :
FEATURE:
OTHER INFORMATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2082
                                                                                                                                                                                                                                                   Local Similarity 55.0%;
nes 115; Conservative
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INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.64
INFORMATION: SWISSPROT HIT: Q60963, EVALUE 2.20e+00
INFORMATION: NT HIT: g115718683, EVALUE 0.00e+00
INFORMATION: EST_HUMAN HIT: AA426355.1, EVALUE 1.00e-114
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al Similarity 100.0%;
166; Conservative
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                                                                                                 GCAGCCTGGGCCCCCGAGCACCCAGCCTCCGCAGGCATGTCCTCATCCATAACACCCTCC
                                                                                                                                TCCCTTCCTATAGCCTGCAGCGACAGTCACTCCTGGACATGTCCCTTGTCAAGCTCCAGC
GGCAGATCCAGGAGGAAATGAGCCAGGAT
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                               AACAGCTGCAGGCTGCACTTCGCCTGGCT 216
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                                                                 TĊTĠTĊACATGĊTAGTGĠAGĊĊĊAATĊŤĊTĠĊĊĠĊTCĠŤĊĊŤĊAŤĊGCCAAĊAĊAGŤĊĊ
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Pred. No. 0.0012;
0; Mismatches 91;
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GENERAL INFORMATION:

APPLICANT: Bayer Aktiengesellschaft
APPLICANT: Hagen, Gustav
APPLICANT: Wick, Maresa
APPLICANT: Zubov, Dmitry
TITLE OF INVENTION: Regulatory DNA Sequences of
TITLE OF INVENTION: Telomerase Subunit, and Th
FILE REFERENCE: LeA 32 805C1
CURRENT APPLICATION NUMBER: US/10/840,455
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: PCT/EP98/08216
PRIOR APPLICATION NUMBER: US 09/582,246
PRIOR APPLICATION NUMBER: US 09/582,246
PRIOR APPLICATION NUMBER: DE19757984.1
PRIOR FILING DATE: 1997-12-24
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US-10-840-455-44/c
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US-10-840-455-20/c
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                                                                                                 APPLICANT: Zubov, Dmitry
TITLE OF INVENTION: Regulatory I
TITLE OF INVENTION: Telomerase
FILE REFERENCE: LeA 32 805C1
CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2004-05-06
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Matches
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Publication No.
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Publication No.
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LENGTH: 3179
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PRIOR PRIOR
                                             PRIOR APPLICATION NUMBER: PCT/EP98/08216
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/582,246
                                                                                                                                                                                                            APPLICANT: Bayer APPLICANT: Hager APPLICANT: Wick,
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                                  PRIOR
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0-840-455-20
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              FILING DATE: 2000-0 APPLICATION NUMBER:
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                                                                                                                                         INVENTION: Regulatory DNA Sequences INVENTION: Telomerase Subunit, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version
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Similarity 50.4%;
39; Conservative
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                                                                                                                                                                                                                                                                                            Application
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                                                                                                                                                                                                           Hagen, Gusta
Wick, Maresa
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               DE19757984.1
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Pred. No. 0.0026
); Mismatches 1
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Their D
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Their Diagnostic and Therapeutic Use
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APPLICANT: Brett P. Monia; APPLICANT: William Gaarde
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                                                                                                                                                                                                                                                                                                                      APPLICANT: William Gaarde
APPLICANT: Susan M. Freier
APPLICANT: Edward V. Wancewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF THE REFERENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
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SOFTWARE: Pa
SEQ ID NO 44
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SEQ ID NO 30
LENGTH: 51552
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(25138)
                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-12-07 PRIOR APPLICATION NUMBER: 09/572,423 PRIOR FILING DATE: 2000-05-16
                                                                                                                                                                                                                ORGANISM:
FEATURE:
NAME/KBY: exon
LOCATION: (21567)..
OTHER INFORMATION:
                                        NAME/KBY: intron
LOCATION: (12951).
OTHER INFORMATION:
                                                                                  NAME/KEY: exon
LOCATION: (11597).
OTHER INFORMATION:
                                                                                                                          LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAME/KEY: intron
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1
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                                                                    NAME/KBY:
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exon 3
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OTHER INFORMATION: i
NAME/KEY: exon
LOCATION: (46130)...
OTHER INFORMATION: e
NAME/KEY: intron
LOCATION: (46255)...
OTHER INFORMATION: i
NAME/KEY: exon
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LOCATION: (41875)...
OTHER INFORMATION: e.
NAME/KEY: intron
LOCATION: (42002)...
OTHER INFORMATION: i.
NAME/KEY: exon
LOCATION: (42882)...
OTHER INFORMATION: e.
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OTHER INFORMATION: NAME/KEY: intron
LOCATION: (36014)...
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (37885)...
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OTHER INFORMATION: e
NAME/KEY: intron
LOCATION: (25550)...
OTHER INFORMATION: i
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OTHER INFORMATION:
NAME/KEY: intron
LOCATION: (31359)...
OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: 31450
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LOCATION: (30293)...
OTHER INFORMATION: i:
NAME/KEY: exon
LOCATION: (31273)...
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OTHER INFORMATION:
NAME/KEY: exon
(25394)..
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LOCATION: (42944)
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LOCATION: (33844).
OTHER INFORMATION:
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LOCATION: (23852).
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: exon
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OTHER INFORMATION:
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OTHER INFORMATION:
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(21763)
                                                                                  intron 13
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intron 1
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; NAME/KEY: exon
; LOCATION: (4771)
; OTHER INFORMATION: US-09-733-294A-30
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LENGTH: 440
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Publication
                                                                                                                    Query Match
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APPLICANT:
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Best Local
                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                          APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                    TYPE:
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OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 1
                                                                                                          Local
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Chen, Jian
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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                          CWSSC.CYRNHCSCC..YNC.MS..YKNSSBC.CY.C..CS.CSCYT.NC.M.GC.MD
                                                                                      7.6%; Score 44.8; DB 5 ilarity 18.8%; Pred. No. 0.0058; Conservative 81; Mismatches 16
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US20030044930A1
ACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTGCCCCCGAGCCCCTC 246
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Pred. No. 0.0038;
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                                                                                                                     DB 5;
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US-10-184-634-
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Smith, Victoria
Watanabe, Colin K
Wood, William I.
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Goddard, Audrey
Godowski, Paul J
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             CDCCSA.WTCSDC.BC.WSCYBTHTCDY.BH.T.YC..DCANC.TDTT.CBYNC.THTTC
                                         AATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCGGTACTTG
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US-10-063-685-52/c
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US-10-063-685-52
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FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 170
SEQ ID NO 52
                                                                                              Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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Baker, Kevin P.
Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-(
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ORGANISM: Homo
10-123-155-10
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Filvaroff, Ellen
Gao, Wei-Qiang
                                Smith, Victoria
Stewart, Timothy A
                                                      Gurney, Austin L. Sherwood, Steven
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Godowski, Paul
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Gurney, Austin
                       Tumas,Daniel
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DeForge, Laura
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LENGTH: 594
TYPE: PRT
                                                                                         APPLICANT: Wood, Wil: APPLICANT: Zhang, Zonitie of invention: Title of invention:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
             Prior Apploication removed - See File Wrapper NUMBER OF SEQ ID NOS: 550
                                         FILE REFERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
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ANT: Beresini, Maureen
ANT: Deporge, Laura
ANT: Deporge, Luc
ANT: Desnoyers, Luc
ANT: Filvaroff, Ellen
ANT: Gao, Wei-Qiang
ANT: Godowski, Paul J.
ANT: Goddard, Audrey
ANT: Godowski, Paul J.
ANT: Gurney, Austin L.
ANT: Sherwood, Steven
ANT: Sherwood, Steven
ANT: Stewart, Timothy A.
ANT: Tumas, Daniel
ANT: Watanabe, Colin K
ANT: Watanabe, Colin K
ANT: Watanabe, Zemin
OF INVENTION: SECRETED AND TRANSMEMBRANE PO
OF INVENTION: ACIDS ENCODING THE SAME
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; TYPE: PRT
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US-10-140-472-10
Search completed: February Job time : 747 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

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Sequence:
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US-11-136-527-150
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US-11-121-086-5
US-11-121-086-101
US-11-121-086-101
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US-11-121-086-101
US-11-043-752-3906
US-11-043-752-3909
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US-11-121-086-2/c

; Sequence 2, Application US/11121086
; Publication No. US20050266459A1
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID PROBES AND NUCLEILE REFERENCE: 09138.6000-00000
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 191684
; TYPE: DNA
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RESULT 2 US-10-502-8 ; Sequence

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TITLE OF INVENTION: Diagnostics and Therapel
TITLE OF INVENTION: Human 5HT6 Receptor
FILE REFERENCS: LeA 35 827
CURRENT APPLICATION NUMBER: US/10/502,893
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: PCT/EP03/000479
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: EP 02001942.8
PRIOR FILING DATE: 2002-02-01
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENETIC P
TITLE OF INVENTION: CARDIOVA
TITLE OF INVENTION: DETECTIO
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2004-11
NUMBER OF SEQ ID NOS: 85702
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Matches
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NAME/KEY: misc
LOCATION: (1)...
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ORGANISM: HOMO
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                                                                                                                                                                                                                                                                              Version 4.
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US-10-995-561-66759, Application US/10995561;
Sequence 66759, Application US/10995561;
Publication No. US20050272054A1;
PITTLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
PITTLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONDENTIAL OF INVENTION: DETECTION AND USES THEREOF
PILE REFERENCE: CL001559;
CURRENT APPLICATION NUMBER: US/10/995,561;
CURRENT FILING DATE: 2004-11-24;
NUMBER OF SEQ ID NOS: 85702
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LENGTH: 2910
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local
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                                                                 SEQ ID NO
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TITLE OF INVENTION: GENE EXPRESSION PROFILING
FILE REFERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
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APPLICANT: HOULGATTE, Remi
APPLICANT: HIRNBAUM, Daniel
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LOCATION: (1)..(2910)
OTHER INFORMATION: cullin 2(CUL2) gene
                                  LENGTH:
TYPE: DI
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
0-995-561-66759
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                                                             FILING DATE: 2004-11-24
F SEQ ID NOS: 85702
: PastSEQ for Windows Version 4.0 66759
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RESULT
US-10-8
                        GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnor
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,04;
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 596
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US-10-995-561-13385
; Sequence 13385, Application US/10995561
; Publication No. US20050272054A1
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Best Local S
Matches 74
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRU
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13385
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 596, A Publication No.
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Mismatches
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RESULT 9
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US-10-821-234-59
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GENERAL INFORMAT
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SOFTWARE: Pate
SEQ ID NO 3584
LENGTH: 2792
        SOFTWARE:
SEQ ID NO 1
LENGTH: 3
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Best Local S
Matches 63
                                                                                                                                                              Sequence 150, Publication No
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                                                                                                               TITLE OF INVENTION:
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                                            NUMBER OF SEQ
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For
FILE REFERENCE: 031896-041000 (AM1010)
TYPE:
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                                            F INVENTION: Probe Arrays For Expression Profiling FERENCE: 031896-041000 (AM101086)
APPLICATION NUMBER: US/11/136,527
FILING DATE: 2005-05-25
PPLICATION NUMBER: US 60/574,294
ILING DATE: 2005-05-26
OF SEQ ID NOS: 362830
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FILING DATE: 2005-05-25
PLICATION NUMBER: US 60/574,294
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PE SEQ ID NOS: 362830
Patentin version 3.2
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US-10-858-730
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Best Loc
Matches
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TITLE OF INVENTION: NUCLEIC ACID PROBES AND FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
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                 APPLICANT
     APPLICANT:
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ORGANISM: Homo
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Trueheart, Jos. Walbridge, Mich
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Doten, Reed
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Driggers,
                                   O'Leary, Jessica
O'Toole, George
                                                                 Madden,
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ilarity 51.9%;
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APPLICANT: HEARD, Jacqueline
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: CREELMAN, Robert
APPLICANT: RATCLIFFE, Oliver
APPLICANT: REPETTI, Peter
APPLICANT: KUMIMOTO, Roderick W
APPLICANT: GUTTERSON, Neal
APPLICANT: GUTTERSON, Neal
APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF
FILE REFERENCE: MBI0058-CIP
CURRENT APPLICATION NUMBER: US/10/714.887
CURRENT FILING DATE: 2003-11
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
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R APPLICATION NUMBER: 09/506,720
R FILING DATE: 2000-02-17
R APPLICATION NUMBER: 60/135,134
R FILING DATE: 1999-05-20
R APPLICATION NUMBER: 09/394,519
R FILING DATE: 1999-09-13
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APPLICATION NUMBER: US 60/475,000
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DATE: 2000-03
ATION NUMBER:
DATE: 2000-03
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TION NUMBER: 09/533,392
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TUMBER: 09/532,591
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WMBER: 09/533,029
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GTCTCGCTTCTTCCCGGCGCGCGTCTGGCCCCCTGCTC 143494

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TITLE OF INVENTION: NUCLEIC ACID PROBES AND FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 101
LENGTH: 185393
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NUMBER OF
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APPLICATION NUMBER: 09/713,
FILING DATE: 2000-11-16
ning Prior Application data
OF SEQ ID NOS: 430
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APPLICATION NUMBER: 6
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APPLICANT: LOTT, STEVE
APPLICANT: CHANDLER, DAWN
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
FILE REFERENCE: UTSC:651US
CURRENT APPLICATION NUMBER: US/11/153,238
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/09/927,091
PRIOR APPLICATION NUMBER: 60/227,560
PRIOR APPLICATION NUMBER: 60/227,560
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ORGANISM: Human
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 9
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PRIOR
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CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: PCT/US04/022446
PRIOR FILING DATE: 2004-07-14
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SOFTWARE: FastSEQ
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NTION: METHODS OF DIAGNOSIS AND TREATMENT FOR
NTION: ASTHMA AND OTHER RESPIRATORY DISEASES
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E: 2345.2044-003
CATION NUMBER: US/11/043,752
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therapy.
                                  The present invention provides the protein and coding sequences of the replication protein A binding transcriptional activator 1 (RBT1). The protein is capable of inducing apoptosis. The sequences are useful in togene therapy and other methods of treatment of cancer, including leukaemias. The present sequence is the RBT1 protein
                                                                                                                                                 Disclosure
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11-JAN-2000;
02-MAY-2000;
                                    The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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N-PSDB;
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11-JAN-2000;
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                                           This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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N-PSDB; ADL32051.
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The invention relates to providing a patient diagnosis for lung cancer comprising comparing the level of expression of genes or gene products in a biological sample from the patient with the level of expression of genes or gene products in a biological sample from a normal individual. Also included are distinguishing between normal and disease tissues, conitoring the response of a patient being treated for lung cancer by administering an anti-cancer agent, identifying a compound useful for the treatment of lung cancer and an array for distinguishing between normal and disease tissues (comprising 2 or more probes corresponding to 2 or more genes selected from any of the 200 nucleotide sequences given in the specification). In providing a patient diagnosis for lung cancer, one or more genes are selected from any of the 200 nucleotide sequences as mentioned in the specification, or one or caid sequences mentioned in the specification. The methods are useful for detecting and treating lung cancer. These may also be used for designing, identifying and optimizing therapeutics for cancer. The present sequence represents a protein from one of the 200 lung cancer marker genes. Note:

The sequence data for this patent did not form part of the printed
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe the hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 Sim:
                                                                                                                                                                                                                                                    genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cited above, an ORF-encoded peptide comprising the single exone cited above, an ORF-encoded peptide comprising at least 8 uous amino acids of any of the above- mentioned amino acid ces (optionally with conservative amino acid substitutions), an ed antibody that binds specifically to a peptide cited above, so f selling and/or licensing single exon probes or microarrays to omer desiring to measure gene expression, a method of providing gene expression data by subscription, and a computer-readable e medium which contains a database having a plurality of records record including data on the expression of a single exon probe above. The probe, methods and apparatus are useful in gene sion analysis. The probes may be used as tools for surveying s to detect the presence of expressed messages that contain their ic exon, or in constructing genome-derived single exon microarrays. Ition, the probes are used in identifying and characterising ative splicing events, in detecting and characterising gross tions in the genomic locus that includes their exon, in assessing r genomic alterations, in priming the synthesis of nucleic acids, expressing the ORF-encoded peptide. The present sequence is a human exon probe protein of the invention. Note: The sequence data for atent did not form part of the printed specification, but was ed in electronic format directly from USPTO at a supprocessing the ORF encoded peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
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                                                                                        2002
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PENN S G.
RANK D R.
HANZEL D K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVFLBALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPBPPHNLFCAPGSWEWNBLDHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPLPC-PPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPLGLQNEVPPQPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sion (comprising a plurality of single exon nucleic acid d above, where each of the plurality of probes is separately ably isolatable or amplifiable from the plurality), a single rray for measuring human gene expression, a method of
                                                                                                                                                                                                                                                                                                                                             andard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPLGLQNEVPPQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity
                                                                                                                                                                                                       expression; single exon splicing event; genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                           2002US-00029386
                                                                                        2002US-00029386.
                                                                                                                                                                                                                                                      derived single exon protein #6308
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 645.5; DB
Pred. No. 9e-55;
D; Mismatches
                                                                                                                                                                                                           probe; microarray;
alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
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190

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RESULT 8
AAY36004
ID AAY3
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AC AAY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes of the plurality), a single exon microarray for measuring human gene expression, a wector comprising the single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of soquences (optionally with conservative amino acid substitutions), an customer desiring to measure gene expression, a method of providing thuman gene expression probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression analysis. The probe methods of single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes and apparatus are useful in gene expression analysis. The probes and apparatus are useful in gene expression analysis. The probes are used in identifying and characterising roses alterative splicing events, in detecting and characterising gross smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression analysis, for identifyi splicing events, for assessing genomic
                                                                                                                      AAY36004
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                  Extended human secreted protein sequence
                                                    13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human
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                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                            MEGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHN
                                                                                                                                                                                                                                                                                                                                                                                                                 111
                                                                                                                                                                                                                                                                           MVGGLKRKHSD
                                                                                                                      standard;
                                                                                                                                                                                                                                       TLOOLOAALRLAPAPALPPEPLFLGEEDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for humession analysis, for identifying or characterizing alternative events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR,
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                    (first entry)
                                                                                                                   protein;
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                                                                                                                                                                                                          PRAPLPGRGGF
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Pred.
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Mismatches 9;
                                                                                                                                                                                                                                                                           PAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHN
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                   SEQ
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ADP19312

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RESULT 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-38
N-PSDB; AAXS
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13-APR-1998;
10-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolate
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                                                                                                                                                                                                                                                                                                               LDTSMDGTEPPQNPVTPLGLQNEVPPQPD----PVFLEAL----SSRYLGDSGLDDFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLKRKREBEBEKEPLAVDSW-WLDPGHAAVAQAPPAVASSSLFDLSVLKLHHSLQXSXPD
                                                                                                                                                                                                                                                                                                                                                           ilarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ge 330-331; 516pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d human secreted proteins.
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                                                                                                                                                                   SMYDNELWAPASEGLKPGPED---GPGKEEAPELDEABLDYLMDVLVGT
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98US-0074121P.
98US-0081563P.
98US-0096116P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 216; DB 2; 32.6%; Pred. No. 1.6e-12; tive 36; Mismatches 69
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                                                                                                                                                                                                                                                                     LADEGPPGRSIGGXPPXLGALDLLGPATGCLLDNGLEGLFE
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                                                                                                                                                                                                                                                                   The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do or do not express the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are sequence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1998;
09-FEB-1999;
21-JUN-2000;
15-SEP-2000;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide encoding secreted polypeptide, useful gene therapy, or in diagnostic procedures to identify individuals genetic diseases resulting from abnormal expression of the genes.
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Similarity 32.6%;
76; Conservative
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                                              L-SHIEC
                                                                                                                                                                                                                                                 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 568; 113pp; English.
                                                                                                LRHLVLVXNTLRRIQAS--MAPAAALPPVPTPPAAPXVADNLLASSDAALSASMAXLLED
                                                                                                                      LRRHVLIHNTLQQLQAALRLAPAPALPPEPL
                                                                                                                                                                         GLKRKHSDLEBEE
                                                                        LDTSMDGTBPPQNPVTPLGLQNBVPPQPD-
DIDTSMYDNELWAPASEGLKPGPED-
                       DIDTSAVEKE-
                                                                                                                                                 GLKRKREEBB
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99WO-IB000282.
2000WO-IB000951.
2000US-00663600.
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                       PARAPPEP-PHNLFCAPGSWE
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                                                                                                                                                                                              Score 216; DB Pred. No. 1.6e 6; Mismatches
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                                               LADEGPPGRSIGGXPPXLGALDLLGPATGCLLDNGLEGLFE
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                                                                                                                                   The present sequence is cell cycle regulation protein-3 (CECRP-3). Prints analytical method was used to identify this protein. CECRPs are activators of cell proliferation or inhibitors of cellular processes that modulate proliferation. They are used to treat or prevent cell proliferative diseases like cancers, atherosclerosis, cirrhosis, hepatitis, psoriasis, immune system disorders (e.g. acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, rheumatoid arthritis). Antibodies are raised to screen for specific binding agents. The corresponding nucleic acid is used in gene therapy, chromosomal
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                                                                                                                                                 and nucleotide sequences of 5'- and 5'-cancer of the full length cDNA are useful been determined. Primers for synthesising the full length cDNA. The full for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did human cDNA of the printed specification, but was obtained in CD-ROM
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K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                           length cDNA
                                                                      DB
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69
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                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuki
                                                                                                                                                                                                                                                                                                                                              full length
 LLRISLDKVQRSLGPRAPS
                                    Indels
                                                                                                                                                                                                                                                                   cDNA molecules have length cDNA are useful
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                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            clones
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T, Koga
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                                   52;
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                                                                                                                                                                                                                                                                                                                              cDNA
isolated
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                    The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For cexample, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the concleic acid molecules may be administered to down regulate GENSET cexpression by binding with the cells' own genes and preventing their cexpression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of cexpression. The sense and antisense nucleic acids may also be used as DNA patients may be in need of restorative therapy. The GENSET polypeptides and be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide of the invention
                                                                                                                                                                                                                                                                                                   proteins, diseases,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-367870,
N-PSDB; AAH64895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                           Claim 21;
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06-MAR-2000;
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                                                                                                                                                                                                                                                                                                   th GENSET human nucleic acids encoding potentially secreted useful in gene therapy and vaccination against a variety o and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                          Page 889-890; 921pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SHIEGLSQAPQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -A2
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2000US-0187470P.
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RESULT 13
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Best Loc
Matches
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11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                            New old
                    encoding proteins that are associated with glycoproteins and transcription. The presen for efficiently cloning a full length human ends using the oligo-capping method. This plength human protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
oligo-
                                                                                                                            This invention relates to a novel primers ulength cDNA molecules that encode human proto secretory or membrane proteins that are target molecules in the field of medicine,
                                                                                                                                                                                                                                                                                                                 WPI; 2004-204755/20
N-PSDB; ADL31643.
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su A, Sugiyama
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Similarity 32.6%;
76; Conservative
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2000JP-00118774.
2000JP-00183865.
2000BP-00114089.
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a T, Nagai
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36; Mis
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                                                                                                                                                                                                                                                                               cDNAs) useful
                                                                                                                                                                                                                                                                                                                                                                       Hayashi K,
K, Kojima
                                                                                                                                               primers useful for synthesising human proteins. Specifically, it that are potential therapeutic a
              curcine, and in particular genes ted with signal transduction, he present invention describes a method gth human cDNA from both the 5' and 3' 1. This polypeptide sequence is a full ion.
                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GPGKEEAPELDEAELDYLMDVLVGT
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AAH99904 encode the human proteins given in the proteins can have activities based on the

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KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;

KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;

KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

KW genetic disease; haematopoietic disorder; platelet disorder; asthma;

KW allergic rhinitis; diabetes; multiple sclerosis; depression;

KW Alzheimer's disease; Parkinson's disease: neurodeceneration;
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Best Loc
Matches
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21-JAN-2000;
25-APR-2000;
                                                        Isolated htreatment
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N-PSDB; AAH99491.
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                                 Page 214; 1217pp; English.
                                                                                                                          Liu C,
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                                                                                                                                            Peptide
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Similarity 32.6%;
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Pred. No. 3.9e-12;
5; Mismatches 69
                                                                                                                                                                                                                                                         protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy;
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ALIGNMENTS

phosphoinositide-3-kinase regulatory beta chain [imported] - human C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C;Accession: H59435; A59436
R;Volinia S; Patracchini P; Otsu M; Hiles I; Gout I; Calzolari E; Bernardi F; R; Oncogene 7, 789-793, 1992
A;Title: Chromosomal localization of human p85 alpha, a subunit of phosphatidyl: A;Reference number: H59435
A;Accession: H59435
A;Accession: H59435
A;Rolecule type: DNA
A;Residues: 1-728 <VOL>
A;Residues: 1-728 <VOL>
A;Cross-references: UNIPROT:000459; UNIPARC:UPI000013106C; GB:NP_005018; PID:941
R;Janssen, J.W.; Schleithoff, L.; Bartram, C.R.; Schulz, A.S.
Oncogene 16, 1767-1772, 1998
A;Title: An oncogenic fusion product of the phosphatidylinositol 3-kinase p85bel
A;Accession: A59436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-728 <JAN>
A;Residues: 1-728 <JAN>
A;Cross-references: UNIPARC:UPI000013106C; GB:NP_005018; PID:94826908; PIDN:NP_005018; PID:94826908; PI RESULT 2
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Chaperonin hsp78p - fission yeast (Schizosaccharom)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: T40514 S B Ş 8 S 밁 Ş H5 Query Match Best Local Matches 4 9435 171 268 224 164 120 60 20 1 Similarity
47; Conserv QWDTAALADGIKSFLLALPAPLVTPEASAEARRALREAAGPVGPALEPPTLPLHRALTLR FL GLQNEVPPQPD---PVFLEALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPEP----NTLQQLQAALRLAPAPALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPL EWSPA----GLQSYQQAL--S -PHNLFCAPGSWEWNEL 186 GAPDGSEPSPDFPALLVEKLLQEHLEEQ--PPSL--QDAEWYWGDI 335 LQHLGRVARRAPA----9.8%; Score 101.5; larity 23.9%; Pred. No. 1; Conservative 25; Mismatches (Schizosaccharomyces pombe) LGPAVRALGATFGPLL--------LRISLDKVQRSLGPRAPSLRRHVLIH DB 2; -EVAPPALPPKPPKAKPAPTVLANGG _005018; PID:g4826908; PIDN:NP_005018.1 70; #text a subunit of phosphatidylinositol Length 728; Indels _change --LRAPPPPSSP-PPG 55; 09-Jul-2004 Gaps PID:g4826908; p85beta F) 119 320 170 9 Rooke

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R;Gwilliam, R.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; submitted to the BMBL Data Library, September 1998
A;Reference number: Z21933
A;Accession: T40514
A;Accession: T40514
A;Accession: DNA
A;Accession: DNA
A;Accession: DNA
A;Cross-references: DNIPROT:074402; UNIPARC:UPI000006C64D; EM
A;Cross-references: UNIPROT:074402; UNIPARC:UPI000006C64D; EM
A;Experimental source: strain 972h-; cosmid c4F6
C;Genetics:
A;Gene: SPDB:SPBC4F6.17c
A;Map position: 2
C;Superfamily: endopeptidase Clp ATP-binding chain
C;Keywords: ATP; molecular chaperone; nucleotide binding; P-1
F;139-146/Region: nucleotide-binding motif A (P-loop)
F;207-212/Region: nucleotide-binding motif B
F;145/Binding site: ATP (Lys) #status predicted
F;545/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                    ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Ara A; Reference number: A86141; MUID:21016719; PMID:11130712

A; Accession: G86441

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1201 < STO>
A; Cross-references: UNIPROT:Q9C6S1; UNIPARC:UPI000009C9CB; GB:AC:Genetics:
A; Map position: 1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C;Accession: G86441
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspice, Theologis, A.; Palm, C.J.; Palm, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federspiel, N.A,
,, A.B.; Conway,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Kaul, S., Wi
A.R., Creasy,
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                                                                                                                                                                                                                             GB: AE005172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-Jul-2004
                                                                           62;
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Maiti, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White, C
                                                                                                                                                                                                                                                                                                                                                                                                                               Sun,
                                                                                                                                                                                                                            NID:g11136725;
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, Dewar,
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Marziali,
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Matches
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A;Cross-references: SGD:S0004329; MIPS:YLR337c
A;Map position: 12R
F;5-14/Region: proline-rich
F;77-85/Region: proline-rich
F;114-180/Region: proline-rich
F;305-336/Region: proline-rich
F;349-357/Region: proline-rich
F;349-357/Region: proline-rich
F;372-382/Region: proline-rich
F;396-406/pe~i--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Munn, A.L.; Stevenson, B.J
submitted to the EMBL Data I
A;Description: end5, end6, a
A;Reference number: S57435
A;Accession: S57435
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;608-621/Region:
F;649-661/Region:
F;678-685/Region:
F;704-710/Region:
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F;421-445/Region:
F;518-528/Region:
F;567-577/Region:
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C; Species: Sa
C; Date: 23-Fe
C; Accession:
R; Du, Z.
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-162, 'F', 164-817 < MUN>
A; Cross-references: UNIPARC: UPI000006B0DE;
A; Experimental source: strain W303
C; Genetics:
A; Gene: SGD: VRP1; MDP5; END5
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A; Residues: 1-81
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A;Description:
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nate names
es: Saccha
23-Feb-19
sion: S513
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96
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                            DKSETVLGMKKAKAPALPGHV-
                                                        DKVQRSLG---PRAPSLRRHVLIHNTLQQLQAALRLAPAPALPPEPLFLGEEDFSLSATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t (Saccharomyces cerevisiae)
s: prolin-rich protein VRP1; protein L8300.13; protein YLR3:
aromyces cerevisiae
.995 #sequence revision 11-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
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ILRELDTSMDGTEPPQNPV-
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he sequence of S. cerevisiae cosmid
                                                                                     Conservative
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                                                                                                                                                                                        proline-rich
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                                                                                   9.3%; Score 96; DB:
25.5%; Pred. No. 3.4;
cive 17; Mismatches
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-TPLGLQNEVP----PQPDPVFLEALSSRYL
                                                                                                                DB 2;
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                                                                                    44;
                              -PPPPVPP----VLSDDSKNNVPA
                                                                                                                Length 817;
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RESULT 6
A54602
microtubule-associated serine/threonine p
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13
C;Accession: A54602
R;Walden, P.D.; Cowan, N.J.
Mol. Cell. Biol. 13, 7625-7635, 1993
A;Title: A novel 205-kilodalton testis-sp
A;Reference number: A54602; MUID:94067123
A;Accession: A54602
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1734 <WAL>
A;Cross-references: UNIPROT:Q60592; UNIPA
C;Keywords: ATP
F;451-726/Domain: protein kinase ATP-bind
F;459-467/Region: protein kinase ATP-bind
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A42029
transcription factor E3 -
C; Species: Mus musculus (
C; Date: 04-Mar-1993 #sequ
C; Accession: A42029
R; Roman, C.; Matera, A.G.
Mol. Cell. Biol. 12, 817-
A; Title: mTFE3, an X-link
A; Reference number: A4202
A; Accession: A42029
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-446 < ROM>
A; Cross-references: UNIPF
A; Note: sequence extracte
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                                                                                                                          Local
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                           80
                                                                                                                                                                                                                                                                                                                                                                             -associated serine/threonine protein
                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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E3, an X-linked transcriptional number: A42029; MUID:92123207; I
                                                                                                           9.1%;
Similarity 26.3%;
51; Conservative
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larity 27.3%;
Conservative
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APSRKHSLDLPHGELKKE
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                                                     PPLGRQLSRPKSAEPPRS
                                                                                --LRISLDKVQRSLGPRAPSLRRHVLIHNTLQQLQAALRLAPAPALPP
                                                                                                                                                                                                                                                                            335, 1993
lton testis-specific serine/threonine
MUID:94067123; PMID:8246979
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                                                                                                            23;
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                                                                                                                                                                homology <KIN>
ATP-binding motif
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                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNIPARC:UPI00000296F2; Lackbone (NCBIN:76673,
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                                                                                                              Mismatches
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                                                                                                                                      93.5;
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TPREASPLBVVGTRSVLSGKGPLPGKGVLQP
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, NCBIP:76674)
                                                                                                                                                                                                           GB:U02313;
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                                                     VQSAEKLAAALAAAB
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C; Species: human T-ce
A; Note: host Homo sal
C; Date: 28-Feb-1986 {
C; Accession: A03944
R; Shimotohno, K; Tal
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A;Title: Complete nucleotide sequence of an infectious clone of human T-cell leukemia A;Accession: A94042; MUID:85216449; PMID:2582407
A;Molecule terms.
RESULT
A82255
                                                                                                                                                                                                                                                                                                                                                          A;Gene: gag
C;Superfamily: mammalian retrovirus gag polyprotein II
C;Keywords: core protein; polyprotein
F;1-136/Product: core protein p15 #status predicted <P15>
F;137-214/Product: core protein p24 #status predicted <P24>
F;215-433/Product: core protein p12 #status predicted <P12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P03346; UNIPARC:UPI000012B002; GB:M10060; A;Note: the authors translated the codon TAC for residues 197 and 249 C;Genetics:
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A;Molecule type: L
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3: core polyprotein
protein p12; core protein p15; core protein
T-cell lymphotropic virus type 2, HTLV-2
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                                                                       -VEPTTTQCFPILHPPGAP----SAHRPWQMKDLQAIKQEVSSS
                                                                                                                                                                                                                                                                                            9.0%; Score 93; DB 23.1%; Pred. No. 2.7; ive 24; Mismatches
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hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: A82255 A; Cross-reference

I.; Sellers,

R.J.

<u>'</u>

A; Experimental C; Genetics: A; Gene: VC0998 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selle l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: A82255

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1621 <HEI> $\boldsymbol{\omega}$ 21 <HBI>
les: UNIPROT:Q9KTA5; UNIPARC:UPI00000C2E4C; GB:AE004181; GB:AE003852;
lource: serogroup O1; strain N16961; biotype El Tor

NID

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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Ske A;Title: Complete genome sequence of a multiple drug resistant Sal A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-804 <PAR>
A;Residues: 1-804 <PAR>
C;Genetics:
A;Gene: STY0554
C;Superfamily: Escherichia coli probable membrane protein ybbP
submitted to the Protein Sequence Dank, Reference number: Z22231
A; Recession: T42644
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-651 < AAA>
A; Cross-references: UNIPROT:09UF93-A; Experiments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
AG0565
probable membrane protein STY0554 [in C; Species: Salmonella enterica subspa; Note: this species has also been car; Date: 09-Nov-2001 #sequence_revision; Accession: AG0565
R; Parkhill, J.; Dougan, G.; James, Kth, T.; Connerton, P.; Cronin, A.; Date: C; Accession: AG0565
                                                                                                     RESULT 10
T42644
hypothetical protein DKFZp566N1047.1 - C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision
C;Accession: T42644
R;Ottenwaelder, B.; Obermaier, B.; Mew
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Similarity 27.4%;
19; Conservative
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    UNIPROT:Q9UF93; 1
ce: fetal kidney;
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Pred. No. 20;
22; Mismatches
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Pred.
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     UNIPARC:UPI000006F0B2; clone DKFZp566N1047
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                                                                                                                                    11-Jan-2000
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                                                                                                         H.W.;
                                                                                             W.; Gassenhuber,
November 1999
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Salmonella
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A;Accession: A56508 A;Status: preliminary A;Molecule type: DNA

09-Jul-2004

encodes a

coiled-coil

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hypothetical prot
C; Species: Caenor
C; Date: 15-Oct-19
C; Accession: T269
R; Wall, M.
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A;Accession: T26998
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-716 <WIL>
A;Cross-references: UNIPROT: Outron
A;Experiment-7
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A; Note: DKF
anucleate primary sterigmata A (apsA) protein - Emericella nidulans C; Species: Emericella nidulans, Aspergillus nidulans C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-00; Accession: A56508 R; Fischer, R.; Timberlake, W.E. J. Cell Biol. 128, 485-498, 1995 A; Title: Aspergillus nidulans apsA (anucleate primary sterigmata) en A; Reference number: A56508; MUID: 95164553; PMID: 7860626
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A;Introns: 38/3;
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larity 24.4%; Pred. No. 12;
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RESULT 13
A34596
transcription factor E3 - human (fra
C; Species: Homo sapiens (man)
C; Date: 06-Jul-1990 #sequence_revisi
C; Accession: A34596; S10379
R; Beckmann, H.; Su, L.K.; Kadesch, T
Genes Dev. 4, 167-179, 1990
A; Title: TFE3: a helix-loop-helix p1
A; Reference number: A34596; MUID: 902
A; Accession: A34596
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-536 <BEC>
A; Cross-references: UNIPROT: P19532;
A; Note: the authors translated the c
C; Genetics:
A; Gene: GDB: TFE3
A; Cross-references: GDB: 125870; OMIN
A; Map position: Xp11.23-Xp11.22
C; Keywords: DNA binding; transcripti
RESULT 14
T14355
protein-tyrosine-phosphatase (
C; Species: Rattus norvegicus (
C; Date: 20-Sep-1999 #sequence_
C; Accession: T14355
R; Cao, L.; Zhang, L.; Ruiz-Loz
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C;Genetics:
A;Gene: apsA
A;Introns: 149/3
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47; Conservative 3
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on: Xp11.23-Xp11.22
DNA binding; transcription factor
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A; Accession: B37761
A; Status: preliminary
A; Molecule type: DNA
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A; Cross-references: UNI
C; Superfamily: Pseudomc
C; Keywords: DNA binding
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A; Title: Complementation of Escherichia coli sigma (54)
A; Reference number: A37761; MUID: 90330545; PMID: 219825
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C;Species: Thiobacillus ferrooxidans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1494 <CAO>
A;Cross-references: UNIPROT:O88902; UNIPARC:UPI00000E5DAD;
A;Experimental source: brain
C;Genetics:
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A; Title: A novel putative protein-tyrosine
A; Reference number: Z18004; MUID: 98361981;
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Q9cwm2
Q4v7a7
Q6nxd9
Q7zz27
Q5rik2
Q14140
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Best Local &
Matches 195
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

STRAIN=C57BL/6J; TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

K MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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K MEDLINE=22388257; PubMed=10.1073/pnas.2426038
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01-FEB-2005 (Rel. 46, Created)

01-FEB-2005 (Rel. 46, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

10-MAY-2005 (Rel. 47, Last annotation update)

SERTA domain-containing protein 3 (Replication practivator) (RPA-binding trans-activator).

Name=Sertad3; Synonyms=Rbt1;

Mus musculus (Mouse).
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EMBL; BC014061; AAH14061.1; -; m
EMBL; BC050643; AAH50643.1; -; m
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HGNC; HGNC:17931; SERTAD3.
InterPro; IPR009263; SERTA.
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PROSITE; PS51053; SERTA; 1.
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the Europuse as loremoved.
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Cho J.M., Alaoui-Jamali M.A.;
"Cloning of mouse RBT1 cDNA.";
Submitted (OCT-2000) to the EM
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Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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TISSUE=Liver;
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Klausner R.D., Coli
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Pfam; PF0603
PROSITE; PS5
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DOMAIN
SEQUENCE
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                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.3%;
ilarity 85.7%;
Conservative 8
188257; PubMed=12477932; DOI=10.1073/pnas.242603899; R.L., Feingold E.A., Grouse L.H., Derge J.G., D., Collins F.S., Wagner L., Shenmen C.M., Schuler
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51053; SERTA;
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886; AAH34886.1; -; mRNA.
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(TrEMBLrel. 30, Last sequence update)
(TrEMBLrel. 30, Last annotation update)
protein MGC108974.
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Pred. No. 9e-59;
8; Mismatches
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Hatting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Loo
Matches
                                                                                                                                             SRTD1 MOUSE STANDARD; PRT; 236 AA.

Q9JL10; Q925E6; Q9D888;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

10-MAY-2005 (Rel. 47, Last annotation update)

SERTA domain-containing protein 1 (Transcriptional reinteracting with the PHD-bromodomain 1) (TRIP-Br1) (Contain protein p34SEI1) (SEI-1).

Name=Sertad1; Synonyms=Sei1;

Mus musculus (Mouse).
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TISSUE=Liver;
NIH MGC Project;
Submitted (MAR-2005) to the EMEMBL; BC091229; AAH91229.1; -;
InterPro; IPR011029; DEATH_lik
InterPro; IPR003139; D_retro m
InterPro; IPR000524; HTH_GntR.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
PROSITE; PS51053; SERTA; 1.
Hypothetical protein.
SEQUENCE 197 AA; 21924 MW;
                                                                Mammalia; Eutheria; E
Muroidea; Muridae; Mu
NCBI_TaxID=10000
     (1) NUCLEOTIDE Ohtani N.,
                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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Murinae; Mus
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Pred. No. 8.9e-5
LO; Mismatches
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhatt N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Grant mouse CDNA services"."
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RUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

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RUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RUCLEOTIC SCALE MRNA [LARGE SCALE MRNA].

RUCLEOTIC MRNA [LARGE SCALE M
                                                                                                                                          Whiting M., He Whiting M., Blakesley R. Rodriguez A. Butterfield Schnerch A., "Generation and mouse cD Proc. Natl.
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                                                                                                                     Proc.
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21231173; PubMed=11331592; DOI=10.1093/emboj/20.9.2273;
., Yang C.M., Sim K.G., Hentschel D.M., O'Leary E.,
                                     cDNA sequences.";

1. Acad. Sci. U.S.A. 99:16899-16903(2002).

10N: Acts at B2F-responsive promoters to integrate signated by PHD- and/or bromodomain-containing transcription rs. Stimulates B2F-1/DP-1 transcriptional activity. Renativity of cyclin D1/CDK4 resistant to the inhibitory efficiency.
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INK4a)
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of the mouse transcriptome based on functional annotation of -length cDNAs.";
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proteins that regulate the transcriptional activity of
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    Interacts with the PHD-bromodomain of TIF1, TRIM28/TIF1B
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EMBL; AF366400; AAK52829.1; -;
EMBL; AF366401; AAK52830.1; -;
EMBL; AK004022; BAB23130.1; -;
EMBL; AK008303; BAB25588.1; -;
EMBL; BC016077; AAH16077.1; -;
Ensembl; ENSMUSG0000008384; MGI; MGI:1913438; Sertad1.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
PROSITE; PS51053; SERTA; 1.
PROSITE; PS51053; SERTA; 1.
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Name=zgc:113340;
Brachydanio rerio (Zebrafish) (
Eukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
NCBI_TaxID=7955;
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NUCLEOTIDE SEQUENCE.
STRAIN=Singapore local strain; TISSUB=Embryo;
STRAIN=Singapore local strain; TISSUB=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler (
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.)
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.
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Craniata; Vertebrata;
Teleostei; Ostariophysi
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Q9UHVZ; Q9BUE7;

10-OCT-2003 (Rel. 42, Created)

13-SEP-2005 (Rel. 48, Last sequence update)

13-SEP-2005 (Rel. 48, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

SERTA domain-containing protein 1 (Transcriptional regimence interacting with the PHD-bromodomain 1) (TRIP-Br1) (Clear the protein p34SEI1) (SEI-1).

Name=SERTAD1; Synonyms=SEI1;

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Elearchontoglires; Primates; Catar:
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Richards S., Wo
Villalon D.K., I
NUCLEOTIDE S
MEDLINE=2004
Sugimoto M.,
Shimamoto A.
"Regulation
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Raha S.S.,
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                   SEQUENCE, INTERACTION WITH CDK4, AND VARIANT ALA-31. 047903; PubMed=10580009; DOI=10.1101/gad.13.22.3027; Nakamura T., Ohtani N., Hampson L., Hampson I.N., A., Furuichi Y., Okumura K., Niwa S., Taya Y., Hara E nof CDK4 activity by a novel CDK4-binding protein, p
                                                                                                                                                                                              Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; AF117959; AAF08349.1; -; EMBL; AF366402; AAK52831.1; -; EMBL; AY130860; AAM77800.1; -; EMBL; BC002670; AAH02670.1; -; EMBL; BC002670; AAH02670.1; -; Ensembl; ENSG00000197019; Homo HGNC; HGNC:17932; SERTAD1. H-InvDB; HIX0015136; -. GO; GO:0008284; P:positive reg GO; GO:000079; P:regulation o InterPro; IPR009263; SERTA.
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PROSITE;
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TISSUE=Uterus;
MEDLINE=22388257; PubMed=12477932; DOI
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Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,

Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,

Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,

Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                             of p16(INK4a).
SUBUNIT: Inter
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prphism; Transcription;
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38
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E.A., Grouse L.H., Derge J.G.,

S., Wagner L., Shenmen C.M., Schuler G

S., Wagner L., Schaefer C.F., Bhat N.K
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L Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
R EMBL; AK223011; BAD96731.1; -; mRNA.
R EMBL; AK222970; BAD96690.1; -; mRNA.
R SEQUENCE 236 An
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eucaryotic |
Gene 138:17
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Eukaryota; N
Mammalia; Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Human small intestine;
Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano
"Construction and characterization of a full length-enri
end-enriched cDNA library.";
Gene 200:149-156(1997).
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NCBI_TaxID=9606;
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Maruyama K.,
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Similarity 32.6%;
76; Conservative 36
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(TrEMBLrel. 31, Last annotation update)
containing 1 variant (Fragment).
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Pred. No. 2.3e-08;
36; Mismatches 69;
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                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 76
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Director MGC Project;
Submitted (NOV-2003) to the E
EMBL; BC061808; AAH61808.1; -
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
SEQUENCE 236 AA; 25419 MW;
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SERTA domain containing 1
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Mammalia; Eutheria; Euarchontoglires; Glires;
Muridae; Murinae; Rattus.
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Last annotation
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Rodentia; Sciurognathi;
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P NUCLEOTIDE SEQUENCE.

C STRAIN=C57BL/6J; TISSUE=Kidney;

X MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsud T., Gissi C., King B., Kochiwa H.,

A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Hayashizaki Y.,

Bollade J., Kamiya M.,

Brownster P.,

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Meth. Enzymo
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Name=Sertadl
Mus musculus
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Q9DCZ2;
Q9DCZ2;
01-JUN-2001
01-JUN-2001
01-MAR-2004
                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUB=Kidney;
STRAIN=C57BL/6J; TISSUB=Kidney;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Hayashizaki Y.
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Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Consortium,
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
s adult male kidney cDNA, RIKEN full-length enriched
one:0610008D10 product:TRIP-BR1, full insert sequence.
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79253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
, Hayashizaki Y.;
iency full-length cDNA cloning.";
ol. 303:19-44(1999).
                                   L/6J; TISSUE=Kidney;
30913; PubMed=110768
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   Itoh M.,
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 PubMed=11076861; DOI=10.1101/gr.152600;
M., Aizawa K., Nagaoka S., Sasaki N., Carninci
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L., Washio T.,
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RESULT 10
Q4T2W4 TETNG
ID Q4T2W4;
AC Q4T2W4;
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT Chromoso
DE (Fragmen
GN ORFNames
OS Tetraodo
OC Eukaryot
OC Actinopt
OC Acanthom
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Matches
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A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Okazaki Y., Susuki H., Tagami M., Tagawa A., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
B Muramatsu M., Hayashizaki Y.;
B Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AK002324; BAB22013.1; -; mRNA.
Q4T2W4;
Q4T2W4;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence
13-SEP-2005 (TrEMBL
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Similarity 25.9%;
57; Conservative
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eostei; Euteleostei; Neoteleos
Percomorpha; Tetraodontiformes
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Neoteleostei
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Watahiki M.,
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RESULT 11
Q4S6F1_TETNG
ID Q4S6F1_T
AC Q4S6F1;
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
Chromoso
DE Chromoso
DE Chromoso
CFragmen
GN ORFNames
OS Tetraodc
OC Actinopt
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OC Acanthom
OC Tetrador
OC NCBI_Tax
RN [1]
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Nature 431:946-957(2004).
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Best Local
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Q4S6F1;
13-SEP-2005
13-SEP-2005
13-SEP-2005
     Anthouard
Biemont C.
Cruaud C.,
                                                                                                                                                    Acanthomorph
Tetradontoid
NCBI_TaxID=9
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Actinopteryç
                                                    Nicaud S.,
Dasilva C.,
                                                                                   Jaillon O.,
Mauceli E.,
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NON TER
SEQUENCE
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Mauceli E.,
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NUCLEOTIDE
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                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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                                                                                                                                                                   nigroviridis (Green puffer).
Metazoa; Chordata; Craniata; Verte
/gii; Neopterygii; Teleostei; Eutel
pha; Acanthopterygii; Percomorpha;
dea; Tetraodontidae; Tetraodon.
                Aury J.M., Brunet F., Petit J.L., Stange-Thomann Bouneau L., Fischer C., Ozouf-Costaz C., Bernot Jaffe D., Fisher S., Lutfalla G., Dossat C., Segui Salanoubat M., Levy M., Boudet N., Castellano S., Jubin C., Castelli V., Katinka M., Vacherie B., Skalli Z., Cattolico L., Poulain J., De Berardin Skalli Z., Cattolico L., Poulain J., De Berardin
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1010161; CAF92768.1;
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(TrEMBLrel. 31, Last annotation update)
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      Coutanceau J.P.,
                                                                                                                                                                                                                                                                                       shotgun sequence.
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                                                                                                                                                                                     Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
rpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -WEWNELDHIMEIILGS
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Matches
                                                                                              Lovell J.;
Submitted (DEC-2004) to the E
EMBL; BX248515; CAI20741.1; -
ZFIN; ZDB-GENE-030131-5926; B
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
NON TER 229 229
SEQUENCE 229 AA; 25097 MW;
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Q5RIK3;
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-!- CAUTION
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    ches
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel protein (Fragment).
Name=si:dkey-177p2.6; Synonyms=OTTDARP00000005081;
ORFNames=DKEY-177P2.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
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J., Roest Crollius H.;
sh Tetraodon nigroviridis
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                                                                       A Okazaki Y., Fruruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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A Hara A., Hashizme M., Waterston R., Lander E.S., Rogers J.,
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Muroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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Eutheria; Euarchontoglires; Gl
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of full-length cDNA clones from mouse brain cDNA library igo-capping method.";
(APR-2000) to the EMBL/GenBank/DDBJ databages
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(Rel. 48, Last annotation update)
n-containing protein 2 (Transcriptional regulator
with the PHD-bromodomain 2) (TRIP-Br2).
2; Synonyms=Kiaa0127; ORFNames=MNCb-1504;
 -length cDNAs. ";
                       Hayashizaki Y.;
f the mouse transcriptome based on functional annotation of
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l. 42, Created)
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lires; Rodentia; Sciurognathi;
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T "Generation and initial analysis of more than 15,000 full-length human rand mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                Query Match
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Matches 77
                                                                                                                                                                                                                                                          EMBL; AB041541; BAA95026.1; -; EMBL; AK076787; BAC36480.1; -; EMBL; BC014726; AAH14726.1; -; EMBL; AF366403; AAK52832.1; -; Ensembl; ENSMUSG00000049800; MGI; MGI:1931026; Sertad2. InterPro; IPR009263; SERTA.
                                                                                                                                               CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                    "TRIP-Br: a novel family of PHD zinc finger- and bromodomain-interacting proteins that regulate the transcriptional activity of E2F-1/DP-1.";
EMBO J. 20:2273-2285(2001).
-!- FUNCTION: Acts at E2F-responsive promoters to integrate signal provided by PHD- and/or bromodomain-containing transcription factors (By similarity).
-!- SIMILARITY: Contains 1 SERTA domain.
                                                                                                                                                                                                                                   InterPro; IPR009263; SERTA
Pfam; PF06031; SERTA; 1.
PROSITE; PS51053; SERTA; 1
                                                                                                                                                                                                                                                                                                                                                                           use
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MEDLINE=21231173; PubMed=11331592; DOI=10.
Hsu S.-I., Yang C.M., Sim K.G., Hentschel
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Bonventre J.V.;
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D.M., O'Leary
                                                                                                                          DB
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                       APAPALPPEPLFLGE-
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RESULT 14
Q5SSE5_MOUSE
ID Q5SSE5;
AC Q5SSE5;
DT 10-MAY-2005
DT 10-MAY-2005
DT 10-MAY-2005
DT 10-MAY-2005
DE Novel protein
GN Name=RP23-45;
OC Mus musculus
OC Musmalia; Euroc
OC Muridae; Muric
OC Mammalia; Euroc
OC Muridae; Muric
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Best Local S
Matches 77
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NCBI_TaxID=10090;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Novel protein similar to cell division cycle associated 4
Name=RP23-452C23.1; ORFNames=RP23-452C23.1-001;
Mus musculus (Mouse).
                                             187
                                                                                             240
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Similarity 24.8%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGG-KRKFDEHEDGLEGKIVSPSDGPSRVSYTLQRQTIFNISLMKLYNHRPLTEPSLQKT
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                                              IMEIILGS 196
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                                                                                                                                                   -PPHNLFCAPG---SWEWNEL
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RESULT 15
Q6GM81_XENLA
ID Q6GM81_XENLA
AC Q6GM81;

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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.
A Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length hu roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                Query Match
Best Local S
Matches 58
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Richardson P.;
"Genetic and genomic tools for initiative.";
The Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                        Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EME
EMBL; BC074195; AAH74195.1; -;
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
SEQUENCE 248 AA; 27319 MW;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MGC82098 protein.
Name=MGC82098;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Yenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
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MEDLINE-22341132;
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184
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Similarity 30.9%;
8; Conservative 7
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                                                     NPVTPLGLQNEVPPQPDPVFLEA-
 TSMYDSDP
                          TSAVEKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=12454917;
sberg R.L., Wagne:
 191
                             163
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-; mRNA.
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                                                                                                                              -APALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOI=10.1002/dvdy.10174; r L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        research:
                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                   58;
                                                                                      LSSRY-
                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The NIH Xenopus
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Mullahy S.J.,
naratne P.H.,
J., Hulyk S.W.,
                                                                        LGDSGLDDFFLDID
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                                                                                                                                                                                                                                   Gaps
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Search completed: February 6, 2006, 10:01:09 Job time : 257 secs

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; Sequence 2, Application US/10076069
; Patent No. 6872812
; GENERAL INFORMATION:
; APPLICANT: JURECIC, ROLAND
; APPLICANT: NACHTMAN, RONALD
; TITLE OF INVENTION: HEPP, A NOVEL GENE WITH A F
FILE REFERENCE: 39532-176599
; CURRENT APPLICATION NUMBER: US/10/076,069
; CURRENT APPLICATION NUMBER: US 60/268,923
; PRIOR APPLICATION NUMBER: US 60/268,923
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
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LENGTH: 237
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; Patent No. 68
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APPLICANT: JURECIC, ROLAND
APPLICANT: NACHTMAN, RONALD
TITLE OF INVENTION: HEPP, A NOV
FILE REFERENCE: 39532-176599
CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 2002-02-1
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                        APPLICANT: HELIX RESEARCH INS
TITLE OF INVENTION: No. 69432
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2002-03
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
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US-09-949-016-891
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; Patent No. 640
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8918
LENGTH: 529
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Best Local
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                  SPPSL--QDAEWYWGDI 345
                                                                                                                                                                                                                                                                                                                                                                       GAPDGSEPSPDFPALLVEKLLQEHLEEQ--
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                                                                                                                                                                                                                                                                                                                                             -PHNLFCAPGSWEWNEL 186
                                                                                                                                             Swanson, Priscilla A. Idler, Kenneth B. Rosenblatt, Joseph D. Chen, Irvin S. Y.
                                                    Robertson, Eugene F. Stephens, John E. Chan, Emerson W. Buytendorp, Mark H. Johnson, Joan E. Motley, Cheryl T.
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ilarity 23.4%;
Conservative 2
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  Guidinger, Pe
Tate, Cynthia
                          Peterson, Bryan
Edwards, Michelle
                                                                                                                                     Golde, David W.
                                                                                                                                                                                                      Lee, Helen
                                                                                                                                                                                          Priscilla A.
            Peggy
                                                                                                                        Eugene F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 95.5; DB 2; Pred. No. 0.72;
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                                                                                                                                                                                                                                                                                                                                                                          -EVAPPALPPKPPKAKPAPTVLANGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71;
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OF DETECTION AND USES
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RESULT 6
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                                                                                                   Patent No. 6858418
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. 685841
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-05-
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                NUMBER OF SOFTWARE:
                                                   PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (708) 938-262 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                      EQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/086
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Daniel W. Collins
REGISTRATION NUMBER: 31,912
REFERENCE/DOCKET NUMBER: 5381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-6365
 ORGANISM: Mus
                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-JUN-
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
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                                                  FastSEQ
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Assays for Detecting
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No.
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0.78;
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US-07-672-483-4
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Query Match
Best Local S
Matches 40
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Best Local
                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: AMINO ACID
                                                                                                                                                      APPLICATION NUMBER: US 07/554
FILING DATE: 18-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: HALLEY Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: IAF8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEPAX: (212)715-0674
TELEX: 14-8367
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-I
SOFTWARE: Patentin Rel
                                                        MOLECULE
7-672-483-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF
                                                                                                                                                                                                                                                                                                 FILING DATE: 1991030
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
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                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
9.0%; Score 93; DB 1; Local Similarity 23.1%; Pred. No. 0.97; les 40; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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o. 5359029
INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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T: ZRBIN, Maan
INVENTION: PEPTIDES
INVENTION: THEREOF
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GSQSFPTKLHLSPPLGRQLSRPKSABPPRSPLLKR-----
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875 Third Avenue
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VIRUSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
 67;
                            Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1734;
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   Indels
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 42;
 Gaps
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US-10-076-069-
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APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for er
TITLE OF INVENTION: heteropolyketide cor
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,8:
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 4
EARLIER FILING DATE: 1998-10-09
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                                    Patent No. 687281
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ENERAL INFORMATION:
APPLICANT: JURECIC, ROLANI
APPLICANT: NACHTMAN, RONI
TITLE OF INVENTION: HEPP,
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Hofle, Gerhard
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Beyer, Stefan
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CURRENT APPLICATION NUMBER: US/10/076,069
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
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10-076-069-6
                                                                           INFORMATION
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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                                                                                                       REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4125PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
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                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                    OPERATING SOFTWARE:
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TYPE: amino acids STRANDEDNESS: unki
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                                               LENGTH:
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T: States of America as represented

T: by the Secretary, Department of

T: Health and Human Services

TINVENTION: ISOLATION AND

INVENTION: CHARACTERIZATION OF A NOVEL PRIMATE T-CELL

INVENTION: LYMPHOTROPIC VIRUS AND THE USE OF THIS VIRUS

INVENTION: OR COMPONENTS THEREOF IN DIAGNOSTIC ASSAYS

INVENTION: AND VACCINES
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ilarity 45.3%;
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22-APR-1994
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RESULT 12
US-09-377-285B-1
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Best Local S
Matches 44
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SOFTWARE: FastSEQ for V
SEQ ID NO 10257
LENGTH: 379
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APPLICANT: VENTER, J.
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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09-949-016-1
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                                                                                                                                                                                                  -EGAAAAAASPTPSEDEEP-
                                                                                                                                                                                                                                                                                                             ; Score; Pred. 23; Mis
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Pred. No. 1.1;
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Mismatches
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                                                                                         Sequence 16, Application US/10192381

Patent No. 6864083

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL APPLICANT: WORLEY, Paul
APPLICANT: TU, Jian
APPLICANT: XIAO, Bo
APPLICANT: LEAHY, Daniel
APPLICANT: BENEKEN, Jutta
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE EN
FILE REFERENCE: JHU1580-4
CURRENT APPLICATION NUMBER: US/10/192,381
CURRENT FILING DATE: 2002-07-09
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US-10-192-381-16
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LENGTH: 37
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APPLICANT:
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APPLICANT: XIAO, Bo
APPLICANT: LEAHY, Daniel
APPLICANT: BENEKEN, Jutta
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER
FILE REFERENCE: JHU1580-4
CURRENT APPLICATION NUMBER: US/09/377,285B
                PRIOR PRIOR
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     DATE: 2002-07-09

OR APPLICATION NUMBER: US/09/377,285

OR FILING DATE: 1999-08-18

OR APPLICATION NUMBER: US 60/138,426

OR FILING DATE: 1999-06-10

OR APPLICATION NUMBER: US 60/138,493

OR FILING DATE: 1999-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR APPLICATION NUMBER: US 60/138,426
OR FILING DATE: 1999-06-10
OR APPLICATION NUMBER: US 60/138,493
OR FILING DATE: 1999-06-10
OR APPLICATION NUMBER: US 60/138,494
OR FILING DATE: 1999-06-10
OR APPLICATION NUMBER: US 60/097,334
OR FILING DATE: 1998-08-18
BER OF SEQ ID NOS: 72
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6
   TION NUMBER:
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60/138,494
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DB 2;

Length 370;

62;

Indels

49;

Gaps

8

--EPLFLG

85

PHNLFCAPG

179

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137

147

265

PROTEIN (AS

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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METH

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/231,401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 312

LENGTH: 824
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US-09-949-002-312
; Sequence 312, Application US/09949002
; Patent No. 6900016
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 370
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-192-381-16
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RESULT
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Best Local S
Matches 43
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Best Local S
Matches 39
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ORGANISM: Human
09-949-002-312
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39; Conservative
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Similarity 23.5%;
43; Conservative 2
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                                                                    SRYLGDSGLDDFFLDIDTSAVEKE---
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                                                                                                                       PEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPLGLQNEVPPQPDPVFLEALS
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                                        PPFPVPVYTRQAPKQVIKPTFAPPVPP
                                                                                                                                                   -LSRNVAPKTTMGRSNPLFH-
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                                                                                                                                                                                                     Pred. No. 3.9;
4; Mismatches
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Pred.
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                                                                                              -VPTTHPG-QPARHPASSVALKR--PPPAPPVTVSS--
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                                                                    PARAPPEPP
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APPLICATION NUMBER.
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
CROUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appring Patent No. 5843721
GENERAL INFORMATION:
GENERAL TOWNS Rothe, Mike
                                                                                                                                                                                                                                                                                        Matches
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Best Local (
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COMPUTER REAL
MEDIUM TYP
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
MOLECULE TYPE
8-887-518-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NIK Proteins, Nucleic Acids
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: C
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                                                      KASOSSRDTLSSGVHSWSSQAEARSSSWN 843
                                                                                                                                                                                                                                 GGLK---SPWRGBYKEPRHPPPNQANYHQ----TLHAQPRELSPRAPGPRPAEETTGRA
                                                                                                                                           PLGLQNEVPPQ-----PDPVFLEALSSRY-----
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APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SII

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO PILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288
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APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SII
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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SEQ ID NO 15
LENGTH: 236
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Best Local S
Matches 76
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Publication No
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OTHER INFORMA
-11-095-870-15
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: MODULATION OF TRIP-BR FUNCTION AND METHOD
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
FILE REFERENCE: 93231-89
CURRENT APPLICATION NUMBER: US/11/095,870
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/557,697
PRIOR PILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 16
                                                                                    APPLICANT: Clusel, Catherine TITLE OF INVENTION: Complementary DNA's EncFILE REFERENCE: 56.US4.CIP CURRENT APPLICATION NUMBER: US/09/978,360A CURRENT FILING DATE: 2001-10-15 PRIOR APPLICATION NUMBER: US 60/066,677
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SOFTWARE: Pate
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          APPLICATION NUMBER: US FILING DATE: 1997-12-1;
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APPLICATION NUMBER: US (
FILING DATE: 1997-12-17
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Duclert, Aymeric
Bougueleret, Lydie
Jobert, Severin
Clusel, Catherine
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Similarity 31.5%;
76; Conservative 3:
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     NUMBER:
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                                60/074,121
                                                            60/069,957
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Pred. No. 2.2e-11;
3; Mismatches 64
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US-09-731-872-412
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                                                                                                         APPLICANT: Dumas Milne Edwards, Jean Bapt:
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN cDNJ
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
                                       NUMBER OF SEQ ID NOS
SOFTWARE: Patent.pm
SEQ ID NO 412
LENGTH: 236
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SEQ ID NO 568
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ORGANISM: Homo
)9-731-872-412
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LOCATION: (28, 30, 40, 67,
OTHER INFORMATION: unknown
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R FILING DATE: 1998-11-13
R APPLICATION NUMBER: US 09/215,435
R FILING DATE: 1998-12-17
R APPLICATION NUMBER: PCT/IB98/02122
R FILING DATE: 1998-12-17
R APPLICATION NUMBER: US 09/247,155
R APPLICATION NUMBER: US 09/247,155
R FILING DATE: 1999-02-09
ining Prior Application data removed
ER OF SEQ ID NOS: 810
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APPLICATION NUMBER: US
FILING DATE: 1998-08-10
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larity 32.6%;
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RESULT 8
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SOFTWARE: Patent.pm
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PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
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9-876-997-412
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Similarity 32.6%; Pred. No. 5.1e-1
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US-11-095-870-14
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CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: US/09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
                                           Query Match
Best Local S
Matches 76
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Best Loc
Matches
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Publication No. US20050222034A1
GENERAL INFORMATION:
APPLICANT: Hsu, Stephen I-Hong
TITLE OF INVENTION: MODULATION OF TRIP-BR FUNCTION AND METHOD
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
FILE REFERENCE: 93231-89
                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 1
LENGTH: 2
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                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: TRI
11-095-870-14
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10-643-836-412
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/095,870 CURRENT FILING DATE: 2005-03-31 PRIOR APPLICATION NUMBER: US 60/557,697 PRIOR FILING DATE: 2004-03-31
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                                                                                                                                             ORGANISM:
FEATURE:
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                           TYPE:
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Pred. No. 5.1e-11;
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RESULT 10
US-10-296-115-106
US-10-296-115-1065,
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PRIOR APPLICATION NUMBER: US09/488,725; PRIOR FILING DATE: 2000-01-21; PRIOR APPLICATION NUMBER: US09/552,317; PRIOR FILING DATE: 2000-04-25; NUMBER OF SEQ ID NOS: 1478; SEQ ID NO 1065; LENGTH: 278
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US-10-029-386-34001
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                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SI
TITLE OF INVENTION: EXPRESSION ANALYSIS TW
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                            Publication No. US20 GENERAL INFORMATION:
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TITLE OF INVENTION: 1
FILE REFERENCE: 784P
                            NUMBER OF SEQ
            SOFTWARE:
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US20040053248A1
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                            ID NOS: 34288
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US20030194704A1
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                                     МВБR: US/10/029,386
2001-12-20
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Pred. No. 6.3e-11;
36; Mismatches 69
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US-10-076-069-
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LENGTH: 23
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Matches 75
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Publication No. US20020177214A1
GENERAL INFORMATION:
APPLICANT: JURECIC, ROLAND
APPLICANT: NACHTMAN, RONALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HEPP, A NOVEL FILE REFERENCE: 39532-176599 CURRENT APPLICATION NUMBER: US/10/CURRENT FILING DATE: 2002-02-15
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TYPE: PRT
ORGANISM: Homo
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Similarity 32.6%;
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                                        SÓVÓSSYYDLDTVLTGMMSGTKSSLCNGLEGFÁAATPPPSSTCKS-
                                                                   LDIDTSAVEKEPAR-
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EXPRESSED IN HELA, SIGNAL = 0.46
SWISSPROT HIT: Q14140, EVALUE 2.
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Pred. No. 2.5e-10;
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         RESULT 14
US-10-755-889-627
; Sequence 627, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND PO
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
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US-10-170-385
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CURRENT APPLICATION NUMBER: US/10/170,385

CURRENT FILING DATE: 2002-06-12

PRIOR APPLICATION NUMBER: PCT/GB02/01662

PRIOR APPLICATION NUMBER: PCT/GB01/05458

PRIOR APPLICATION NUMBER: PCT/GB01/05458

PRIOR FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 549

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
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SEQ ID NO 3
LENGTH: 3
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Similarity 22.7%; Pred. No. 0.007;
71; Conservative 34; Mismatches 88
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CATION
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NUMBER: US/10/755,889
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-CAPGSWEW

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US-11-095-870-12
; Sequence 12, A
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PRIOR APPLICATION NUMBER: U.S. 60
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version 3.2
SEQ ID NO 627
LENGTH: 314
TYPE: PRT
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Matches 71
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                                                                                               OTHER INFORMATION: TRIP-Br2
                                                                                                                                                                                                                      APPLICANT: Hsu, Stephen I-Hong
TITLE OF INVENTION: MODULATION OF TRIP-BR FUNCTION AND
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
FILE REFERENCE: 93231-89
CURRENT APPLICATION NUMBER: US/11/095,870
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/557,697
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.3
                                                                                                                                      FEATURE:
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                                                                                                                                                                   ORGANISM:
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Similarity 22.7%;
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71; Conservative :
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                           EGGLKRKHSDLEESESRWEWSPAGLQS--
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ER: U.S. 60/440,068
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Pred. No. 0.007;
34; Mismatches
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GENERAL INFORMATION: GARNATION GENERAL INFORMATION: APPLICANT: Edwards, Jean-Baptiste Dumas Milne APPLICANT: Boldert, Aymeric APPLICANT: Boldert, Aymeric APPLICANT: Boldert, Swerin APPLICANT: Glusel, Catherine TILLO FINVENTION: Complementary DNA's Encoding Proteins with Signal Peptides TILL DOF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides TILL REFERENCE: 56, US4.CIP CURRENT PILING DATE: 1997-11-13 PRIOR APPLICATION UNDERE: US 60/066.677 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION UNDERE: US 60/069.957 PRIOR FILING DATE: 1997-12-17 PRIOR APPLICATION UNDERE: US 60/069.957 PRIOR APPLICATION UNDERE: US 60/069.957 PRIOR APPLICATION UNDERE: US 60/069.957 PRIOR APPLICATION UNDERE: US 60/069.116 PRIOR APPLICATION UNDERE: US 60/069.273

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RESULT 3
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US-10-511-722-1
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Publication No
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.:
SEQ ID NO 19
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APPLICANT: Yeda Research and Development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 149217
PRIOR FILING DATE: 2004-10-15
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 152183
PRIOR FILING PAGE
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CURRENT APPLICATION
CURRENT FILING DATE
                           APPLICANT: Wallach, David
APPLICANT: Shmushkovich, Taisia
APPLICANT: Ramakrishnan, Parameswaran
TITLE OF INVENTION: Derivatives of the
FILE REFERENC
CURRENT APPLI
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Similarity 25.8%; Pred. No. 0.24;
34; Conservative 17; Mismatches
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  NUMBER:
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Matches 50
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Sequence 1657, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1657
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LENGTH: 324
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2004-0
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TITLE OF INVENTION: Methods
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Similarity 25.8%;
64; Conservative
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Sequence 4, Application US/10964313;
Publication No. US20050287629A1
GENERAL INFORMATION:
APPLICANT: GROZINGER, CHRISTINA M.
APPLICANT: HASSIG, CHRISTIAN A.
APPLICANT: SCHREIBER, STUART L.
TITLE OF INVENTION: CLASS II HUMAN HISTONE DE.
TITLE OF INVENTION: THERETO
FILE REFERENCE: HUV-037.02
CURRENT APPLICATION NUMBER: US/10/964,313
CURRENT FILING DATE: 2004-10-13
PRIOR APPLICATION NUMBER: 09/800,187
PRIOR APPLICATION NUMBER: 60/186,802
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
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US-10-964-313-4
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NUMBER OF SEQ ID NOS
SOFTWARE: PatentIn v
SEQ ID NO 217
LENGTH: 1015
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SEQ ID NO 4
LENGTH: 1122
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Best Local S
Matches 50
                                                                                                                                                                                                                                         Sequence 217, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER FILE REFERENCE: 10001 NP CURRENT APPLICATION NUMBER: US/11/169,041 CURRENT FILING DATE: 2005-06
                                              CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
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ORGANISM: HO
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Similarity 24.4%; Pred. No. 1.7;
50; Conservative 23; Mismatches
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; ORGANISM: HOUS-11-169-041-21

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TYPE:

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; Sequence 990, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHI
; TITLE OF INVENTION: CARDIOVASCULAR DI
; TITLE OF INVENTION: DETECTION AND USE
; FILE REFERENCE: CL001559
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LENGTH: 1823
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 20.7%;
15; Conservative 1
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              Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED
CARDIOVASCULAR DISORDERS AND DRU
DETECTION AND USES THEREOF
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Pred. No.
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US-10-995-5
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Best Local S
Matches 45
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 989
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                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Homo sapiens
10-995-561-990
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ORGANISM: Homo
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Similarity 20.7%; Pred. No. 10;
45; Conservative 18; Mismatches
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LGAVPAPQAPPPPKALYPGALGRPPPMPPMNFDPRWMM--IPPYVDPRLLQGRPPLDFY
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AVPAPQAPPPPPKALYPGALGRPPPMPPMNFDPRWMM--IPPYVDPRLLQGRPPLDFY 689
TSPLRQAADEDDKGMRSETPPVPPPPPPY-LASYPG
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                           -LDIDTSAVEKEPARAPPEPPHNLFCAPG 179
                                                                                                                                            -LRELDTSMDGTEPPQNPVT--PLGLQNEVPPQPDPVFLB--
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; ORGANISM: Homo US-10-857-780-23
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US-10-857-780-23
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; ORGANISM: Homo
US-10-995-561-991
                                                                                                                                                                                     APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RITITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
                                                                                                            SOFTWARE:
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Query Match 7.9%;
Best Local Similarity 27.1%;
Matches 45; Conservative
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Best Local
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                    PRIOR FILING DATE: 2003-0 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2003-1
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Similarity 20.7%;
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KAMMERER, STEFAN M.
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RES
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US-11-134-5
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APPLICANT: Campellone, Kenneth G.
TITLE OF INVENTION: ESPFU NUCLEIC ACTITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07917-280001
FILE REFERENCE: 07917-280001
TOTREENT APPLICATION NUMBER: US/11/1
2005-05-20
                  NUMBER OF SOFTWARE: SEQ ID NO 10
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                                                                                                           PRIOR APPLICATION NUMBER: US/09/976,059
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/239,924
PRIOR FILING DATE: 2000-10-13
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                               FILE REFERENCI
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No. US20050287569A1
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APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-00
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       NENT FILING DATE: 2002-01-22

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OR APPLICATION NUMBER: 60/263,598

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OR APPLICATION NUMBER: 60/263,799

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Baumgartner, Jason
Shimkets, Richard
Cusev, Vladimir
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Ratelli, Luca
Rekuda, Ramesh
Kekuda, Kamesh
Guo, Xiaojia
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Miller, Charles
Miller, Velizar
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Gerlach, Kimberly
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Taupier Jr., Ra
Pena, Carol
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Ballinger, Rober
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Mezes, Peter
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Burgess, Cahterine
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